STIC-Biotech/ChemLib

Seharaseyon, Jegatheesan Thursday, July 12, 2001 10:37 AM STIC-Biotech/ChemLib 09/554,933

From: Sent: To: Subject:

Please search SEQ ID No: 3 of 09/554,933. Thanks.

J.Seharaseyon Art Unit 1647 CM1 10D16 10CO1 MB (703)-305-1112 THIS PAGE BLACK (USPTO)

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: An Unit: Phone Nur		Examiner #:	Date:
Art Unit: Phone Nur Mail Box and Bldg/Room*Location:	mber 30	Serial Number:	PAPER DISK F-MAII
Mail Box and Bidg/Room Location:	Kesui	its Politial Preferred (circle).	TAI ER DIOR E-MAIL
If more than one search is submitt	ed, please prioritize	e searches in order of ne	ed.
Please provide a detailed statement of the sea Include the elected species or structures, key utility of the invention. Define any terms tha known. Please attach a copy of the cover she	arch topic, and describe a words, synonyms, acrony at may have a special me	s specifically as possible the sub ms, and registry numbers, and c aning. Give examples or relevan	ject matter to be searched.
Title of Invention:			
Inventors (please provide full names):			
Earliest Priority Filing Date:			
For Sequence Searches Only Please include appropriate serial number.	all pertinent information (parent, child, divisional, or issued p	atent numbers) along with the
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Date Searcher Picked Up: 7/12/0/	Bibliographic	Dr.Link	
Date Completed: 7/16/0/	Litigation	Lexis/Nexis	
Searcher Prep & Review Time:	Fulltext	Sequence Systems	502
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Online Time: 2 m	Other	Other (specify)	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC AAY13344-403 represent secreted and transmembrane human proteins.
CC The cDNA sequences are obtained from cDNA libraries, prepared from cC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
CC The encoded polypeptides have specific uses based on their homology to common polypeptides, e.g. PRO211 and PRO217 can be used for disorders cassociated with the preservation and maintenance of gastrointestinal cc mucosa and the repair of acute and chronic mucosal lesions
CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal cc ulceration and congenital microvillus atrophy), skin diseases associated cwith abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), content effects on cell growth and development, diseases related to concert such or survival of nerve cells including parkinson's disease, acc Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as confirmed to anti-thromodulin, e.g. for reducing dermal scarring. PRO264 can be used cas a target for anti-tumor drugs. PRO533 may be used in the treatment cc of Usher Syndrome or Atrophia areata; PRO269 can be used as an enti-thrombotic agent; PRO287 polypeptides and portions may have cc used for treating problems of the kidney, uterus, endometrium, blood cvessels, or related tissue, e.g. in the heart of genital tract.
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Best Local :
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gastrointestinal ulceration
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DB; AAX52261.
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Pred. No. Be-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human; chromosome 12.
                                                                                                                                                                                                                                                                                                                    antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and antagonists may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermattitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory disorders e.g. inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                    in AAA80606-A80623 encode the 12 secreted protein sequences given in AAB25576-B35593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological;
                                                                                                                                   hyperproliferative disorders such as paraproteinaemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #10 and protein sequences are represented in sequences AAAB06615 and AAB25585. Secreted protein gene #10 is located on ohromosome 12. Sequences AAB25616-B25618 represent alternative secreted protein #10 sequences and AAAB0669-A80676 represent genes which are related to the secreted protein gene#10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606-A80623 encode the 12 secreted protein sequences given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases
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 The present invention relates nucleotide sequences encoding
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                                  Disclosure;
                                                        Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer wounds, and infectious diseases.
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Best Local 9
                                                                             TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185; TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; mur secreted protein; transmembrane protein; gene therapy; vaccine;
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                                           diagnosis;
                                                                                                                                                                                                                                                                                Human TANGO 186 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY88277 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2000
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                                           treatment;
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Pred. No. 8e-147;
D; Mismatches 0;
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CC proteins) which can be used for gene therapy and/or vaccination. The cc peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic cc acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215. The nucleic cc polypeptides according to standard recombinant DNA methodologies. They cc may also be used to detect and quantify the presence of TANGO nucleic cacids in a sample and therefore identify or diagnose diseases associated cc with inappropriate TANGO expression (e.g. diseases related to over or cc under expression of the polypeptides or the expression of inactive polypeptides). The nucleic acids and the polypeptides they encode may be used according to standard gene therapy protocols, to treat diseases cc associated with inappropriate TANGO expression by supplementing a patients own production of the polypeptide of to rectify mutations that cm may result in expression of an abnormally active polypeptide. The colypeptides may also be used to identify and produce agonists and cantagonists of TANGO expression and activity which may be used to complete the polypeptides are particularly useful for use as antigens for producing antibodies comproteins in samples and therefore identify patients in whom the protein is over- or under-expressed. This sequence represents the human crown that the polypeptide of the polypeptides of the polypeptides are particularly useful for use as antigens for producing antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Fig 13; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with inappropriate protein expression -
Sequence
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02-OCT-1998;
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DB; AAA39945; AAA39946.
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 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                        ktyvkgtqklrvgflkpkfkdggrgandstsampeqmkfqwirvkrthvpkgwikgnand
                                  KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                                                                vssscgpqchkgtplptyeeakqylsyetlyangsrtetqvgiyilsssgdgaqhrdsgs 120
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                      100.0%; Score 2080; DB 2
100.0%; Pred. No. 8e-147;
                                                                                                                                                                                                             0:
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                 DB 21; Length 383;
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                        240
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diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisease, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or antagonists, in competitive drug screens, and for purification of HSPP features.

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                         Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; parkinson's disease; Huntington's disease; ovulatory defect; muscrilar disease;
                                                                                                                                                                                                                                                                           26-JUN-1998;
31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
                                                                                                                                                                                                                                Lal P, T
Akerblom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human signal peptide containing protein HSPP-47 SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY87270 standard;
                                                                                                                                                   New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease –
                                                                                                                                                                                         WPI; 2000-160673/14.
N-PSDB; AAZ98155.
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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H, Patterson
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son C, Reddy
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R, Hillman
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Best Local Similarity
                                                  Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopolesis; anaemia; myeloid cell deficiency; myeloid cell; erythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hematopoedyboinuria; bone growth; cartilage; tendor ligament; nerve; wound healing; tissue repair; burn; incision; ulcone fracture; cartilage damage; artificial joint.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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          Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt vssscgpqchkgtplptyeeakqylsyetlyangsrtetqvgiyilsssgdgaqhrdsgs}
                                                                                                                                                                                                                                                                                                                                                                    TYDLLYQQCDAQPGASGSGYYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
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                                                                                                                                                                                                                                                                                                                                                      {\tt tydllyqqcdaqpgasgsgvyvrmwkrqqqkwerkiigifsghqwvdmngspqdfnvavr}
                                 sapiens
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                                                                                                                                                                                  secreted protein designated BMS192.
  Location/Qualifiers
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be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's

Peptide

AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can

have

Claim 1;

Page 192-193;

327pp;

English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY53622-43 represent bone marrow secreted proteins of human bone marrow CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, CC deficiencies. In addition, they may be used to support the growth and CC proliferation of erythroid progenitor cells, and to treat various CC anaemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as CC granulocytes, monocytes or macrophages, to prevent or treat CC myelo-suppression, to support the growth and proliferation of reatment CC of platelet disorders such as thrombocytopenia, to support the growth and proliferation or treatment CC and proliferation of hematopoeitic stem cells, either in place of or in CC conjunction with platelet transfusions, to treat stem cell disorders, or to crepopulate the stem cell compartment after irradiation or chemotherapy. CC tendon, ligament, or nerve tissue, as well as for wound healing and CC tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR PR XXX PR XXX
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Best Local Similarity
Matches 383; Conserv
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24-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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98US-0102540.
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Pred. No. 8e-147;
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Filvaroff E, For
Godowski PJ, Gr:
Mather JP, Pan (
Williams PM, Woo
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26-JUL-1999
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18-SEP-1999
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29-NOV-1999
30-NOV-1999
30-NOV-1999
20-DEC-1999
20-DEC-1999
20-DEC-1999
20-JAN-2000
                                              Sixty one nucleic acids encoding PRO polypeptides which are useful the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease)
                                                                                                WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory; antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic; antirhemmatic; cancer; antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; cohemic, ifference therapy; skin disease; gastrointestinal disorder;
                            Claim 1; Fig 96; 393pp; English.
                                                                                                                                                                                       (GETH ) GENENTECH INC.
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                                                                                                2001-081051/09.
DB; AAF72419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                     Botstein D, Desnoyers L,
Fong S, Gao W, Gerber H,
Grimaldi CJ, Gurney AL, H
                                                                                                                                                                                                                                                                                                                                                               2000WO-US04414.
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99WO-US30095.
99WO-US30911.
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99WO-US21547.
99WO-US23089.
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99US-0145698.
99US-0146222.
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Stewart TA,
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Kljavin I
Tumas D;
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The present sequence is one of sixty one transmembrane PRO polypeptides. The PRO p

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                alcohol production; laundry detergent
                                                                                                                                                                                         Human Zsig13; serine protease; chromosome 11q22.1; elastase homologue; glutamyl endopeptidase homologue; factor X homologue; trypsin homologu
                                                                                                                                                                                                                                                                                                                AAB48974 standard;
24-APR-1997;
17-APR-1998;
                                         04-MAY-1998;
                                                                                                                                                                trypsinogen homologue;
collagenase homologue;
                                                                                                                                                                                                                                 Human Zsigl3 variant #3, SEQ
                                                                   28-NOV-2000
                                                                                                                      Homo sapiens
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97US-0044185
98US-0062142
                                         98US-0072384.
                                                                                                                                                                                                                                                                                                                   Protein;
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                                                                                                                                                                mast cell protease homologue; protein degradation; food pro-
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Pred. No. 8e-147;
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                                                                                                                                                    component
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27-MAR-2001 AAB48973;

(first entry)

AAB48973 standard;

Protein;

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RESULT 1
AAB48973
ID AAB4
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AC AAB4
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AC AAB4
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AC A7-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human Zsigl3 proteins (AAB48972-B48974), and to DNA encoding them (AAC91782-C91784). The invention also relates to expression vectors and host cells comprising a human Zsigl3 DNA, and t recombinant production of a human Zsigl3 protein or its precursor. Zsigl3 is a serine protease, and has significant homology to Bacillus Zsigl3 is a serine protease, and has significant homology to Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated serine protease (designated Zsig13), useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing composition, as well as in industrial applications
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)B; AAC91784.
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                                                                                                                                                                                                                                                                                       \verb|ktyvkgtqk|| rvgflkpkfkdggrgandstsampeqmkfqwirvkrthvpkgwikgnand||
                                                                                                                                                                                                                                                                                                    KTYVKGTQKLRVGELKDKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                                                                      ITPLKYAQICYWIKGNYLDCREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383;
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Pred. No. 8e-147;
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Human Zsigl3; serine protease; chromosome 11q22.1; elastase homologue;

Human Zsigl3 variant #2,

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Best Local
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N-PSDB; AAC91783.
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17-APR-1998;
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                                                                                                                                                                      SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
                                                                                                                                                                                                                                                                                                                                            IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
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                                                ktyvkgtqklrvgflkpkfkdggrgandstsampeqmkfqwirvkrthvpkgwikgnand
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98US-0062142.
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Pred. No. 8.3e-147;
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     CC which encode human secretory or membrane proteins represented by

CR AAB8317 - AAB8419, Included in the invention are primers

CR AAF3917 - AAF4295 and AAF62232 - AAF62235 which are used to isolate the

CR CAAF3917 - AAF4295 and AAF62232 - AAF62235 which are used to isolate the

CR CDNA sequences of the invention. The invention also includes methods for

CR the production of antibodies directed against the proteins, and cDNA

CR sequences, which can be used in vaccines. The polynucleotide sequences

CR can be used in gene therapy. The polynucleotide sequences and the

CR proteins they encode may be used in the prevention, treatment and

CR diagnosis of diseases associated with inappropriate secretory

CR protein/membrane protein expression. The nucleic acids and complementary

CR sequences may also be used as DNA probes in diagnostic assays

CR (e.g. polymerase chain reactions (PCR)) to detect and quantitate the

CR proteins they expression and function of secretory proteins/membrane

CR polymetides and their role in metabolism. The polypeptides may be used

CR as antigens in the production of antibodies against them and in assays to

CR dientify modulators (agonists and antagonists) of expression and

CR activity. The antibodies and antagonists may also be used as diagnostic agents for detecting the presence of the

CR polypeptides in samples (e.g. by enzyme linked immunosorbant assay

CR (ELISA). Examples of diseases which may be treated include rheumatoid

CR arthrite and dishates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development - {\sf res}
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
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11-JAN-2000;
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rheumatoid arthritis; diabetes
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2000JP-0118775.
2000JP-0183766.
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XX QX

Sequence

383

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Query Match Best Local

Similarity

99.7%; 99.7%;

Score 2073; Pred. No. 2

.7e-146 В

Conservative

0;

Mismatches

Indels Length

Gaps

0;

60 60

383; 0;

Matches

A

protein-containing composition, as well as in industrial

applications

(e.g. brewing)

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RESULT
ARAB48972
ID ARAB
XX ARAB
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N-PSDB; AAC91782.
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17-APR-1998;
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            protease
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                (designated :
d proteins or
            proteins
            Zsig13), useful in industr calter the characteristics
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industrial eristics of

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CC to DNA encoding them (AAC91782-C91784). The invention also relates to CC expression vectors and host cells comprising a human Zsig13 DNA, and the CC expression vectors and host cells comprising a human Zsig13 DNA, and the CC excombinant production of a human Zsig13 protein or its precursor. CC Zsig13 is a serine protease, and has significant homology to Bacillus C1 icheniformis glutamyl endopeptidase, human clotting factor X, human CC licheniformis glutamyl endopeptidase, human clotting factor X, human CC trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human CC zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial CC protein-containing compositions. It may also be used in industrial CC protein-containing compositions. It may also be used in industrial CC applications in which proteases are utilised, including food processing, bearing and alcohol production, and as a component of a laundry CC detergent. The present sequence represents a human Zsig13 variant.
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Matches 377; Conserv
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                    antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; crebic disease;
Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myoc
                                                                                Secreted protein; immunosuppressant; anti-inflammatory;
                                                                                                                                          21-NOV-2000
                                                                                                                                                                                                   AAB25585 standard;
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                                                                                                                                                                                                                                                                                  ITPLKYAQICYWIKGNYLDCREG
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                                                                                                              encoded by human secreted protein gene #10.
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       myocarditis; cancer;
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ITPLKYAQICYWIKGNYLDCREG

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AAB48972

standard;

Protein;

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Human Zsigl3 variant

#1, SEQ

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NO:2.

homologue;

27-MAR-2001

(first entry)

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VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120

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                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to 12 secreted human proteins and t nucleotide sequences encoding them. The polynucleotide sequences in AAA80606-A80623 encode the 12 secreted proteins sequences given AAB25576-B35593. The human secreted proteins have various activit dependent on the tissues in which they are expressed. Examples of activities of the proteins include: immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greene JM;
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                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                        MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE 60
                                                                                                                                                      VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGTYILSSSGDGAQHRDSGS 120
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)B; AAA80615.
KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                  sgksrrkrqiygydsrfsifgkdfllnypfstsvklstgctgtlvaekhvltaahcihdg
                                                                                                                                    vssscgpqchkgtplptyeeakqylsyetlyangsrtetqvgiyilsssgdgaqhrdsgs 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   healing; human; chromosome 12.
                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                          Score 1909.5; DB 2
Pred. No. 3.6e-134;
5; Mismatches 7;
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                                                                                                      The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606-A80623 encode the 12 secreted protein sequences given in AAB25576-B35593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antiheumatic, dermatological; antiproliferative; antiarthritic; antiheumatic, dermatological; antiviral; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and antagonists may be used to treat prevent and conditions of activity are activity.
                                                  and/or diagnose various disease, disorders and conditions examples which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer melanoma; lymphoma; wound healing; human; chromosome 12.
e.g. inflammatory bowel disease, Crohn's disease and nephritis; hyperproliferative disorders such as paraproteinaemias and purp cardiovascular disorders e.g. coronary arteriosclerosis and myo
                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                     used for the prevention, amelioration inflammatory, hyperproliferative and cwounds, and infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cance:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein;
                                                                                                                                                                                                                                                                                                                   Page 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MS
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Matches 354; Conserv
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399 eitplqy 405
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                                                                                                                                                                                                                                                                                        413 AA;
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96.5%;
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Perfect score:
Sequence:
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1 MAGIPGLLFLLFFLLCAVGQ.....LKYAQICYWIKGNYLDCREG 383
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Gapop 10.0 , Gapext 0.5
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Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

g g	Result		ery tch	Length	В	ID	Description
	_	2080	100.0	383	4	US-09-072-384-18	Sequence 18, Appl
•	N	2080		392	4	-09-072-384-1	e 1
	ω	2044		392	4	-09-072-384-2	e 2,
	4	177	8.5	222	-	-08-090-048-	1, Appl
	Ŋ	177		222	N	US-08-292-550-1	1, Appl
	σ	177		222	N	-661A	Sequence 1, Appli
	7	122		256	ω	-769-8	e 89, App
	ω	122		256	4	1	е 89, Арр
	9	122		256	4	-795-8	89,
	10	122		256	4	-075A-	89,
	11	122		256	4	US-09-012-431-89	
	12	122	٠	256	4	US-09-032-215-32	32,
	13	122	٠	256	4	-692-8	89,
	14	122	5.9	256	4	-613-	89, App
	15	122	•	256	Ų,	PCT-US95-14442A-89	89,
	16	11		437	_	037-	2,
	17	115.5		241	4	US-08-944-483-59	59,
	18	114	•	228	4		44, App
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	21	113	٥. 4	250	6	5223425-4	No.
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	23	112.5	5.4	223	_	33-859-1	_
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	25	٠	5.4	223	ນ	-08-487-167-1	13,
	26	112.5	5.4	223	N	-80	13,
	27	112.5	5.4	223	N	US-08-296-149-13	13,

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-08-484-558-1	-042)-978-1	-592	8-484-558-	-042	-978	S-08-774-592-4	-558	-08-474-042	-08-330-978-4	-09-106-467-13	-466	-09-106-468-	-659	-660	-271	4
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ALIGNMENTS

SASE POLYPEPTIDES SAND METHODS FOR Persion 2.0 384

Query Match Best Local

Local Similarity mes 383; Conserv

100.0%; Score 2080; DB 4; ilarity 100.0%; Pred. No. 4.6e-223; Conservative 0; Mismatches 0;

Length Indels

383; 0;

Gaps

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US-09-072-384-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
TITLE OF INVENTION: AND MATERIALS AND METHODS FOR
NUMBER OF SEQUENCES: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1201 E
CITY: Seattle
STATE: WA
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                                                                  TELEFAX:
                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
                                                                              TELEPHONE: 206-442-6673
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAGIPGLLELLEFILCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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RESULT 3
US-09-072-384-2
; Sequence 2, Application US/09072384
; Patent No. 6153420
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,384
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                        APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES.
TITLE OF INVENTION: AND MATERIALS AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
                                                                                                       COMPUTER: IBM COR
OPERATING SYSTEM:
                                                                                                                                                                 COUNTRY: UZIP: 98102
                                                                                                                                                                                                     STREET: 1201 F
                                       CLASSIFICATION:
                                                       FILING DATE
                                                                                                                                                                                             STATE:
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STREET: 1201
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DATE
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01 Eastlake Avenue East
                                                                                                                                     Diskette
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Pred. No. 4.8e-223;
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360 360 300 300 240

240

180

ATTORNEY/AGENT INFORMATION:

NAME: Parker, Gary E REGISTRATION NUMBER:

31,648

MEDIUM TYPE:

Floppy disk

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RESULT 4
US-08-090-048-1
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OTHER INFORMATION:
US-09-072-384-2
                                                                                                                                                                                                         Sequence 1, Application US/08090048 Patent No. 5523237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.3%;
Best Local Similarity 98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Mudtz, Peter
APPLICANT: Midles, Pet M.
APPLICANT: Midles, Por M.
TITLE OF INVENTION: PROTEIN PREPARATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55232370 No. 5523237disk of No. 5523237th America,
ADDRESSEE: No. 55232370 Avenue, 62nd Floor
COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 206-442-6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                               361
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     COUNTRY: United
ZIP: 10174-6201
                                            STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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READABLE
                               United States of
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internal
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FORM:

    Mismatches

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                                America
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Pred. No. 4.9e-219;
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; MOLECULE TYPE:
US-08-090-048-1
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                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.5%; Score 177; DB 1; Length 222; Best Local Similarity 25.5%; Pred. No. 1.6e-11; Matches 60; Conservative 27; Mismatches 104; Indels
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dambmann, Cla
APPLICANT: Budtz, Peter
APPLICANT: Mortensen, S:
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
OPERATING SYSTEM: PC-DOS/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-867-0298 INFORMATION FOR SEQ ID NO: 1:
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APPLICATION NUMBER: PCT/DK
APPLICATION NUMBER: PCT/DK
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,08
REFERENCE/DOCKET NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 199/91
FILING DATE: 06-FEB-1991
                                                                                                                                                                                                                CORRESPONDENCE
                                                                                                                                                                                                                                                          TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
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                                                                                                                   STREET: 405 Lexii
CITY: New York
STATE: New York
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 YPFSTSVKLST---GCTGTLVAEKHVLTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGG 203
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/090,048
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                                                                                                                                                                      405 Lexington Avenue,
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    PC-DOS/MS-DOS
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                                                                                                                                                                      Suite 6400
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SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:

US/08/292,550

APPLICATION NUMBER: FILING DATE: 18 AU

18 AUG 1994

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     equence 1, Application US/07927661A atent No. 5866357
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NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/927,624
FILING DATE: 31 AUG 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/0068
FILING DATE: 8 MAR 1991
                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                        COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58863570 No. 5866357d1sk of No.
                                                                                                                                                                                                                                                                                       APPLICANT: Budtz, Pe
APPLICANT: Eriksen,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                -927-661A-1
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APPLICANT: Mortensen, Steen
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Local Similarity 25.5%;
hes 60; Conservative 2
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TYPE: amino acid
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                                                                          COMPUTER:
APPLICATION
                                                                                                                                                                                                             STREET:
                                                                                          MEDIUM TYPE:
                                                                                                                                                                      New York
                                                                                                                                                                                                           405 Lexington Avenue
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                                                                        IBM Compatible
NUMBER:
                                                                                              Diskette
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US/07/927,661A
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Pred. No. 1.6e-11;
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Patent No. 6077687
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: AGI15, Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3396
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                 CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUTTITLE OF INVENTION: MOLECULES AND USES THEREOF NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
CLASSIFICATION:
                                                                                                                                                                      COUNTRY: USA
ZIP: 80203
                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                   FILING DATE:
                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
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: Colorado
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1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                   Silver, Gary
                                                                                                                                                                                                                                                                                                                                                                                                     Stiegler, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grieve, Robert B. Rushlow, Keith E.
                                                                                                                                                                                                                                                                                                                                                                                   Gaines, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                        Frank, Glenn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu Hunter, Shirley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%; Score 177; DB 2; Length 222; 25.5%; Pred. No. 1.6e-11;
                                     us/08/906,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Mismatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SSYNRGTRITKEVFDNLTNW 217
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APPLICATION NUMBER: US 08/639,075 FILING DATE: 24-APR-1996

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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
           CLASSIFICATION: 536
ATTORNEY/AGENY INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Silver, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                           APPLICATION NUMBER: US/0 FILING DATE: 05-AUG-1997
                                                                                                                                                                                                                                                              STREET: 1700 Lincoln Street, Suite CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                             COUNTRY:
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NUMBER:
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                                                                                             US/08/906,616
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2618-25-C2-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 89,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND TITLE OF INVENTION: PROTEASE VACCINES TO PROTEASE TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE TITLE OF INVENTION: MOLECULES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
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                  ATTORNEY/AGENT INFORMATION
                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                    ADDRESSEE: Sheridan KOSS & FLATELL STATE: 1700 Lincoln Street, Suite 3500 CITY: Denver STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 RIHF-----SGYDNDRPGNLVY 292
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                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                        CLASSIFICATION:
                                                                                                         FILING DATE:
                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                               MEDIUM TYPE:
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                                                                                                                                                                                                                                                     80203
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6139840
Gary J. Connell
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Stiegler, Gary
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24.1%;
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Pred. No. 2.8e-05;
0; Mismatches 68
                                                                                                                                                              Version #1
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-817-795-89
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Best Local Similarity
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US-08-639-075A-89
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
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ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
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                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                             E: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaines, Patrick J.
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                                                                                                                                                                                                                                                                                                                                                                                                                         FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gary
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Pred. No. 2.8e-05;
- ***smatches 68;
                                        2618-25-C2
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US-09-012-431-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 89, Application US/09012431 Patent No. 6180383 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
             TELEFAX: (303) 8 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 VGIYILSS--SGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLST 158
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                                                                                                                                                                                                                                                                  ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC -DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHTLA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                              NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                    APPLICATION NUMBER: US 08/639,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Grieve, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP---HKRKFMKIGVSPPAKQLPGG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CGASILNNYWIYTAAHCIYDEFTY-----SVRVG---TSFQ-GRRGSVHPXAQIIKHPA 100
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                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGLSAVSSYKIKDGLDGRIVGGQDADIAK---YGYQASLQVFNEHF----
SEQUENCE
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amino acid
                                                                                                                                                                                                             APPLICATION NUMBER: US/09/012,431 FILING DATE: 23-Jan-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sheridan Ross & McIntosh STREET: 1700 Lincoln Street, Suite 3500
                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Silver, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stiegler, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu Hunter, Shirley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rushlow, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frank, Glenn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GNVTDI--DMEXALIKVRRPFRLNNRTVRTVKLTDVGKDMPSG 142
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                                                    (303) 863-9700
                                     863-0223
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No. 2.8e-05;
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTINE READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOWNTER: IBM PC DOS/MS-DOS
                                                                                                                                     TELEFAX: (303) 863-02 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS
SOFTWARE: ASCII DOS TEXT
CURRENT APPLICATION DATA:
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acid
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
                    FEATURE:
                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NERAL INFORMATION:
APPLICANT: Stiegler, Gary L.
APPLICANT: Gaines, Patrick J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 RIHF-----SGYDNDRPGNLVY 292
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                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/OFFILING DATE: 27-FEB-1998
                                                          TOPOLOGY:
                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
NAME/KEY: Xaa - any amino acid
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
                                                                        amino acid
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                                                                                          256 amino acids
                                                                                                                                                       (303)
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                                                          linear
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                                                                                                                                                                           (303)
                                      Protein
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                                                                                                                                                                       863-9700
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: maino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-012-692-89
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US-09-032-215-32
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                      APPLICATION NUMBER: US.08/639
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2611
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                       TELEFAX: (303) 863-02 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,692
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Denver
STATE: Colora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
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les 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -CGASILNNYWIVTAAHCIYDEFTY-----SVRVG---TSFQ-GRRGSVHPVAQIIKHPA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Silver, Gary
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                                                                                                                                           (303)
                                                                                                                       863-0223
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24.1%; Pred. No. 2.8e-05;
ative 30; Mismatches 68
                                                                                                                                           863-9700
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                                                                                                        89:
                                                                                                                                                                            2618-25-C2
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Query Match Best Local : Matches 4:

Local Similarity

Conservative

30;

Mismatches

68;

56;

Gaps

10;

5.9%;

Score 122; DB 4; Pred. No. 2.8e-05;

Length 256; ; B; Indels

101 VGIYILSS--SGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLST 158

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; MOLECULE TYPE: US-08-906-613-89
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                                                                                                         TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/906,613 FILING DATE:
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                                     TOPOLOGY:
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                                                  amino acid
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Frank, Glenn R.
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                                                                  ; TOPOLOGY: 1:
; MOLECULE TYPE:
PCT-US95-14442A-89
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Best Local
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Query Match
Best Local Similarity
                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442A
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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NAME: Gary J. Connell
REGISTRATION NUMBER: 32,
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                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                     LENGTH: 250 COUNTY DE: amino acid
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                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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Similarity 24.1%;
49; Conservative 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I: Stiegler, Gary
I: Stiegler, Gary
INVENTION: USE OF PROTEASE INHIBITORS AND
INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
INVENTION: INFESTATION, AND FLEA PROTEINS, NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colorado
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1700 Lincoln Street, Suite 3500
                                                                                                                                     256 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                       (303 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dale, Beverly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arfsten, Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamaka, Miles Yamanaka
                                                                                                                                                                                                       (303) 863-9700
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 5.98;
24.18;
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Pred. No. 2.8e-05;
 Score 122; DB 5;
Pred. No. 2.8e-05;
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                     Length 256
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Mai	Matches	49; Conservative 30; Mismatches 68; Indels 56; Gaps 10;
Qy	101	SGKSF
Ъ	89	VGLSAVSSYKIKDGLDGRIVGGQDADIAKYGYQASLQVFNEHF 50
Qy	159	159 GCTGTLVAEKHYLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMK 218
Ъ	51	51 -CGASILNNYWIVTAAHCIYDEFTYSVRVGTSFQ-GRRGSVHPXAQIIKHPA 100
Qy	219	219 FQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGG 275
망	101	101 YGNVTDIDMEXALIKVRRPFRLNNRTVRTVKLTDVGKDMPSG 142
9	276	276 RIHFSGYDNDRPGNLYY 292
뮹	143	143 ELATVTGWGNLGEDEDDPEQLQY 165

Search completed: July 12, 2001, 11:43:10 Job time: 240 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2001, 11:40:15 ; Search time 15.96 Seconds (without alignments) 1827.998 Million cell updates/sec

Title: Perfect score: Sequence: US-09-554-933-3
2080
1 MAGIPGLLFLLFFLLCAVGQ.....LKYAQICYWIKGNYLDCREG 383

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

arched: 219241 segs, 76174552 residues

Potal number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	s	4	ω	N	1	NO.	Result
103.5	105	107.5	107.5	108	108	108	109.5	110	110	110	111	111.5	112.5	112.5	112.5	113	113	114	114.5	115	115	115.5	115.5	117	119	120.5	135.5	194	Score	
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271	274	686	236	1047	786	583	405	1582	492	269	761	488	273	273	259	266	266	246	238	267	258	271	269	522	269	482	313	316	Length	
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ELRT2	S40004	A59271	A28566	A55617	A47547	A29154	T35117	T15308	EXBO	C26823	JC5759	EXHU	H64915	E85765	TRSMG	ELPG	ELRT1	DBHU	TRWV5Y	A56615	S70439	A25528	B26823	T29767	A26823	EXRT	A35122	A45134	ID	
pancreatic elastas	trypsin-related pr	Ra-reactive factor	T-cell suppressor	masquerade precurs	serine proteinease	complement factor	probable secreted	hypothetical prote	coagulation factor	pancreatic elastas	brain-specific ser	_		ical	trypsin (EC 3.4.21	pancreatic elastas		complement factor	trypsin-like prote	probable pancreati			el	hypothetical prote	pancreatic elastas	coagulation factor	3	endopeptidase (EC	Description	

45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30
94	95	95.5	96.5	96.5	96.5	97	97.5	97.5	97.5	98	98	98.5	100	102.5	103.5
4.5	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.9	5.0
268	782	430	2145	275	259	1019	747	452	409	624	548	267	272	1238	416
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S68825	T32155	A24702	JC4747	146712	S68424	A38738	151579	A30351	T35118	T02289	D82175	S40006	JC4170	T34929	KFBO
pancreatic elastas	hypothetical prote	serine proteinase	adenylate cyclase	factor IX - rabbit	allergen Der f III	coagulation factor	complement factor	coagulation factor	probable secreted	probable polygalac	probable trypsin V	trypsin (EC 3.4.21	. trypsin-like prote	hypothetical prote	coagulation factor

ALIGNMENTS

μ ω ά	290 234	D QQ
	y 230 PKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGN 289 	y Q
æ võ	y 171 LTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPE@MKFQWIRVKRTHV 229	Ф
6 O	Y 120 SSGKSRRKRQIYGYDSRFSIFGKĎFLLNYPFSTSVKLSTGCTGTLVAEKHV 170 	Qy Db
- w	y 63 SSCGPQCHKGTPLPTYEEAKOYLSYETLYANGSRTETOVGIYILSSSGDGAQHRDSG 119	Qy db
15;	Query Match 9.3%; Score 194; DB 2; Length 316; Best Local Similarity 24.0%; Pred. No. 1.2e-08; Matches 79; Conservative 43; Mismatches 143; Indels 64; Gaps	
,	92155199	CPPPPP
785) endopentidase	CBI backbone (NCBIN:118784, NCBIP:118 92 sequence of a diutamic acid specific	<u> </u>
); PID:g21626	A;Accession: A43134 A;Accession: Peliminary A;Molecule type: DNA A;Residues: 1-316 <kak> A;Residues: 1-316 <kak> A;Cross-references: GB:D10060; NID:g216263; PIDN:BAA00949.1; PID:d1001415; A;Cross-references: GB:D10600; NID:g216263; PIDN:BAA00949.1; PID:d1001415; A;Experimental source: ATCC 14580</kak></kak>	22222
:-1999 Okamoto, H.; S	.4), glutamate-specific - Bacillus licheniformi licheniformis sequence_revision 18-Nov-1994 #text_change 15-Oct; #sequence_revision 18-Nov-1994 #text_change 15-Oct; \$23078 hi, N.; Kitadokoro, K.; Fujiwara, T.; Nakamura, E.; 23782-23788, 1992 on, characterization, cloning, and expression of a A45134; MUID:93054737	A A J R C C C C e A A B J R C C C C C e E A A B J R C C C C E E E E E E E E E E E E E E E

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A;Molecule type: DNA
A;Residues: 1-60,65,/L,67,'S,69,'AQA' <RES>
A;Cross-references: GB:M22916; NID:g143701; PIDN:AAA22832.1; PID:g143702
A;Cross-references: GB:M22916; NID:g143701; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Broo, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, A.; Galler
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, A.; Galler
A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,
A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sckiguchi, J.; Sckowska, A.; Seror
Akeuchi, M.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A; Reference number: A69580; MUID:98044033
A.; Reference number: A69580; MUID:98044033
A.; Accession: A69660
A. Statis - nrolliminary: nucleic acid sequence not shown; translation not shown
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ene 70, 351-361, 1988
ritle: Characterization of signal-sequence-coding regions selected
reference number: I39994; MUID:89108019
A;Accession: I40010
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
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A;Title: Gene encoding a novel extracellular metalloprotease in Bacillus subtilis.
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C; Species: Bacillo
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A;Residues: 1-313 <SLO>
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                                                                    В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: A35122; I40010; A69660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12018.1; PID:e1182176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                             130 IYGYDSRF---
                                                                        136 VNPNTVVTAGHCVYSQDHGWASTITAAPGRNGSSYPYGTY-
                                                                                                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                VAEKHVLTAAHCIH--
                                                                                                                                                                                                                                                                                                                                                                                                        GTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGD--GAQHRDSGSSGKSRRKRQ 129
                                                                                                                                                                                                                     LYGGQTELEKNIQTLQPSSIIGTDERTRISSTTSFPYRATVQLSIKYPNTSSTYGCTGFL
                                                                                                                                                                                                                                                                                                                                                              GVPAKAAENPQTSVSNTGKEADATKNQT-----SKADQVSAPYEGTGKTSKS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-313 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 135.5;
Pred. No. 0.(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence not shown; translation not shown
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                                                                                                                                                DGKTYVKGTQKLRVGFLKPKFKDGGRGAND
       -ANDIGMDYDYALLELKKPHKRKFMKIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.00091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 313;
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                   265
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A; Reference number: A58498; MUID:96093366
A; Rocession: S49075
A; Molecule type: mRNA
A; Residues: 1-482 <STA1>
A; Rosidues: 1-482 <STA1>
A; Rosidues: Teferences: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
A; Rote: submitted to the EMBL Data Library, June 1994
A; Note: neither the complete nucleic acid sequence nor the complete translation R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A; Title: Processing and expression of rat and human clotting factor-X-encoding (A.) Reference number: JC4670; MUID:96194815
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       F;41-179/Product: coagulation factor X light chain #status predicted <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F;183-482/Product: coagulation factor X heavy chain #status predicted <ACT>
F;183-231/Domain: activation peptide #status predicted <APT>
F;183-2482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F;232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F;232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F;232-460/Domain: trypsin homology <TRY>
F;46,47,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F;46,47,56,59,60,55,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 183-186, 'X', 188-207 <ENU72>
R; Murakawa, M.; Okamura, T.; Kuroiwa, M.;
Eur. J. Haematol. 52, 162-168, 1994
A; Title: Analysis of the partial nucleotide sequences
A; Reference number: 146196; MUID:94222160
A; Accession: 162745
A; Accession: 162745
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A; Residues: 1-482 <STA2>
                                                                                                                                                                                                                                                                                                                                           F;24-40/Domain: propeptide #status predicted <PRO>F;25-84/Domain: Gla domain homology <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 183-186, 'X', 188-207 <ENJ2>
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A; Residues: 41-58, 'X', 60-65 < ENJ1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number:
A; Accession: PS0191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Pathway: blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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176 -SGTMFYSVK-GWTESKDTNYDYGAIKLNGSPGNTVGW-YGYRTTNSSSP------VGL
                                                                                                                                            SPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMW 325
                                       KROQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW 372
-NGG-SSYNLGTRVTNDVFNNIQYW 310
                                                                                                     --SAETYKLTY-TTDTYGCQSGSPVY---- 272
                                                                                                                                                                                                                     225
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C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 factor Xa (EC 3.4.21.6) precursor -PS0190; I6 Wallin, R. 162745 #text_change 08-Dec-2000 for

nor the complete translation are

CDNAS

A; Cross-references: EMBL: X79807; NID: g506600; PIDN:CAA56202.1; PID:g506601

A; Title: Characterization of rat factors X and A; Reference number: PS0190; MUID:92041742 Xa: demonstration of factor Xa in rat

Harada, M.;

and

deduced

primary structures

Niho,

A;Molecule type: DNA
A;Residues: 295-383,'G',385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu F;I-23/Domain; signal sequence #status predicted <SIG> A; Description: catalyzes the proteolytic activation of prothrombin to thrombin

in the

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F;103/Modified site: erythro-beta-nyuncaries.
F;187/Binding site: carbohydrate (Asn) (covalent) #status experiment.
F;208/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218/Binding site: Arg-Ile (coagulation factor IXa, coagulation
F;201-232/Cleavage site: His, Asp, Ser #status predicted
RESULT 5
T29167
hypothetical protein 2C581.6 - Caenorhabditis
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-
C;Accession: T29767
C;Accession: B; Gattung, S.; Le, T.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-269 < KAM>
A; Residues: GB:M16651; NID:g164441; PIDN:AAA31027.1;
C; Superfamily: trypsin; trypsin homology
C; Reywords: hydrolase; serine proteinase
F; 1-16/Domain: signal sequence #status predicted < SIG>
F; 11-28/Domain: propeptide #status predicted < PRO>
F; 29-269/Product: elastase II #status predicted < MAT>
F; 29-262/Domain: trypsin homology < TRY>
F; 29-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreatic elastase II (EC 3.4.21.71) precursor - pig
N;Alternate names: pancreatopeptidase E
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change :
C;Accession: A26823
R;Kawashima, I; Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA 6, 163-172, 1987
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les 60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQIYGYDSRFSIFGKDFLLNYPFSTSVKL-STG-----CTGTLVAEKHVLTAAHCIHDGK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVVGGEDARPN--
                                                                                                                                                                                                                                                                                                                                                                           DIGMDYDYALLELKKP-HKRKFMKIGVSPPAKQ-LPG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TY--VKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAN 239
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                                                                                                                                                                                                                              QGQLL----VVD----
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                                                                                                                                                                                                                              YATC-SKPGWWGSTVKTNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---DFDIAMLRLKTP 329
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Pred. No. 0.02
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 119; DB 2
Pred. No. 0.018;
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                                               15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                     A;Cross-references: GB:M1652; NID:g182057; R;Fletcher, T.S.; Shen, W.F.; Largman, C. Biochemistry 26, 7256-7261, 1987
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                                            A; Reference number: A27432; A; Accession: A27432
                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-269 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                          pancreatic
C; Species:
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C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988
C;Accession: B26823; A27432; A41431; S34491
R;Kawashima, I; Tani, T.; Shimoda, K.; Takiguchi,
A; Reference number: A; Accession: B26823
                     A; Title: Characterization of pancreatic elastase A; Reference number: A90958; MUID: 87217962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1
A: Introns: 36/2;
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A; Accession: T29767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: AF003134; PIDN: AAB54144.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                412 KTIIGVLSQTSCQKRRGGNETMELYSSVGFYKNQI----CKYTGIC
                                                                 shima, I.; Tani, T.;
163-172, 1987
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                                                                                                                                                                                                                                                                                                                                                                                     PMEIYFFQARDITDKTVACVVSLKILILNKTQASLNISLKGDSGGGAIADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KKPHKR---KFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY------
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                                                                                                                                                                             elastase II (EC 3.4.21.71) A precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 117;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- ANRIKKIPPQYYTDDFAIVHLYEELTFSSNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TYVKGTQKL--RVGFLKPKFKDGGRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153;
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                                                                                                                                   #text_change
                                                                                         ۲.
                                              cDNAs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPDB:GN00019; CESP:ZC581.6
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                                                                                                                                                                                                                                                                                                453
                                              two
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                                              elastase
                                                                                                                                     20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292
                                              II mRNAS
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mRNA

or numan pancreatic MUID:88107669

elastase

N

determined

by sequence

PIDN: AAA52380.1;

PID:g182058

are

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A:Cross-references: GB:D00236; NID:g219619; PIDN:BAA00165.1; PID:g219620 A:Note: the authors translated the codon GTG for residue 202 as Cys R:Moulard, M.; Michon, T.; Kerfelec, B.; Chapus, C. FEBS Lett. 261, 179-183, 1990
A:Title: Further studies on the human pancreatic binary complexes involving A:Reference number: S08253; MUID:90169111
A:Accession: S34491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Map position: 12pter-12qter

Superfamily: trypsin; trypsin homology

Keywords: hydrolase; pancreas; serine proteinase

1-16/Domain: signal sequence #status predicted <SIG>
F:17-28/Domain: propeptide #status predicted <PRO>
F:29-269/Product: pancreatic elastase IIA #status predicted
F:29-269/Domain: trypsin homology <TRY>
F:73,121,216/Active site: His, Asp, Ser #status predicted
                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-271 <STE>
A; Cross-references: GB:X04573; NID:g50825; PIDN:CAA28242.1;
A; Cross-references: GB:X04573; NID:g50825; PIDN:CAA28242.1;
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase
F; 1-30/Domain: signal sequence #status predicted <SIG>
F; 31-271/Product: pancreatic elastase II #status predicted
F; 31-264/Domain: trypsin homology <TRY>
F; 75,123,218/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-201, 'V', 203-269 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M16631; NID:g182022; PIDN:AAA52374.1; PID:g182023 R;Shirasu, Y.; Yoshida, H.; Matsuki, S.; Takemura, K.; Ikeda, N.; Shimad J. Blochem. 102, 1555-1533, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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A; Accession: A25528
                                                                                                                                                                                                                                                                                                                                                         A; Title: Sequence organisation and transcriptional regulation A; Reference number: A93646; MUID:87066713
                                                                                                                                                                                                                                                                                                                                                                                                     R;Stevenson, B.J.; Hagenbuechle, O.;
Nucleic Acids Res. 14, 8307-8330, 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            noreatic elastase II (EC 3.4.21.71) precursor species: Mus musculus (house mouse)
Date: 30-Jun-1988 #sequence_revision 30-Jun-1988
Accession: A25528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GDB:119866; OMIM:130120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: GDB:ELA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: protein Residues: 'X',18-50 <M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 NYPFSTSVKLSTG-----CTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GRHNLYVAESGSLA-----VSVSKIVVHKDW---NSNQISKGNDIALLKLANPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKRKFMKIGVSPPAKQ-LPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGGRG----ANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLTDKIQLACLPPAGTILPNNYPCYVTGWGRLQTNGAVPDVLQQGRLLVVDYATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWPWQVSLQYSSNGKWYHTCGGSLIANSWVLTAAHCISSSRTY-----RVGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                        5.6%;
25.0%;
       38;
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  Score 115.5; DB
Pred. No. 0.036;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Wellauer,
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                                                 DB 2;
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       80;
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                                                                                                                                                                                                                                                                PID:g50826
                                                      271;
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       83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                      mouse elastase
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C;Specie
C;Date:
C;Access
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A; Residues: 1-258 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreatic elastase I (allele HEL1-16) probable splice form I - C;Species: Homo sapiens (man) C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change C;Accession: $70439
                            Qy
                                                              Вþ
                                                                                           δλ
                                                                                                                             멍
                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                           C;Superfamily: trypsin; trypsin homology F;19-251/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A56615; A; Accession: S70439
                                                                                                                                                                                                                                                                                                                                                                                                       R;Kawashima, I.; Tani, T.; Mita-Honjo, DNA Seq. 2, 303-312, 1992
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                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Genomic organization
                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                          Matches
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                                                                                             199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42
124 NSYVQLGVLP
                                258 RKFMKIGVSP
                                                                81
                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVKDETY----DLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNIQTACLPPAGTILPRNYVCYVTGWGLLQTNGNSPDTLRQGRLLVVDYATCSSASWWGS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVKSSMVCAGGDGVTSSCN---GDSGGPLNCRASNGQ---WQ--VHGIVSFGSSLGCN-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP-HKR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPWQVSLQVLSSGRWRHNCGGSLVANNWVLTAAHCLSNYQTYRVLLGAHSL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PODENVAVRITPLKYAQICYWIKGNYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFMKIGVSPPAKQ-LPGGRI-HFSGY-----DNDRPGNLV---YRFC-----
                                                                                                                               SWPSQISLQYRSGGSWYHTCGGTLIRQNWVMTAAHCVDYQKTFRVVAGDHNL-----
                                                                                             FKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL-KKPHK 257
                                                                                                                                                                                               35;
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                             5.5%;
                                                                                                                                                                                                                                                                                                                                                                          on of the human homologue of MUID:92338395
                                                                                                                                                               -CTGTLVAEKHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPK 198
                                                                -QYVSVQKIVVHPYW---NSDNVAAGYDIALLRLAQSVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - VQVSKLVVHQRW---NSQNVGNGYDIALIKLASPVTLS 136
                                                                                                                                                                                             23;
                                                                                                                                                                                                              Score 115; DB 2
Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYID
                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262
                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-Aug-1998 #text_change 16-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                          Shimoda-Takano, K.; Ohmine, T.; Furukawa
                                                                                                                                                                                                                               2;
                                                                                                                                                                                                   38;
                                                                                                                                                                                                                              Length 258
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                           the rat pancreatic elastase
                                                                                                                                                                                                   34;
                                                                                                                                                                                                   Gaps
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                                                                                                                                    80
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C;Species: Homo sapiens (man)
C;Date: 11-Aug-1995 #sequence_revision 17-Aug-1995 #text_change 14-Aug-1998
C;Accession: A56615; S70440
C;Accession: A56615; S70440
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-267 < KAN>
A; Residues: 1-267 < KAN>
A; CHANA
A;
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A;Title: Genomic organization of the human A;Reference number: A56615; MUID:92338395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable pancreatic elastase (EC 3.4.21.36) pseudogene - human N; Alternate names: pancreatic elastase I homolog; pancreatic elastase I allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .; Mita-Honjo, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimoda-Takano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homologue
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A; Nolecule type: mRNA
A; Residues: 1-238 <KAL>
A; Residues: 1-238 <KAL>
A; Residues: 1-238 <KAL>
A; Cross-references: EMBL:X64363; NID:g5563; PIDN:CAA45715.1; PID:g5564
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; insect midgut; protein digestion; serine proteinase
C; Keywords: hydrolase; insect midgut; protein digestion; serine proteinase
C; Keywords: hydrolase; acquence and propeptide (fragment) #status predicted
complement factor D (EC 3.4.21.46) precursor [validated] - human N;Alternate names: adipsin; C3 convertase activator C;Species: Homo sapiens (man) C;Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change C;Accession: A40197; A00936; A60571; S66645 R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.;
                                                                                                                                  DBHU
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F;38-54,162-178,189-213/Disulfide bonds: *status predicted F;53,97,193/Active site: His, Asp, Ser *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S19891
C;Accession: S19891
R;Kalhok, S:; Tabak, L.M.; Prosser, D.E.; Downe, A.E.R.; White, B.N.
submitted to the EMBL Data Library, February 1992
submitted to the EMBL Data Library and characterization of 2 cDNA clones coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
TRWV5Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trypsin-like proteinase (EC 3.4.21.-) 5G1 precursor - yellow fever mosquito C;Species: Aedes aegypti (yellow fever mosquito) C;Datc: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
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A;Map position: 12
C;Keywords: hydrolase;
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Best Local Similarity
"-+>hes 35; Conserv
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S19891
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Best Local S
Matches 42
                                                                                                                                                                                                                                                            265 VSPPAKQLP---GGRIHFSGYDN
                                                                                                                                                                                                                                                                                                                                                                                                                                       149
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                                                                                                                                                                                                                      VKLPQKDTPVNEGTCLQVSGWGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSYVQLGVLP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKFMKIGVSP 267
                                                                                                                                                                                                                                                                                                                                               ANDSTSAMPEQMKFQWIRVKRTH-VPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIG 264
                                                                                                                                                                                                                                                                                                                                                                                          PFQVSLSGVGSSHFCGGSLLSERWVMTAGHCAASGQTNL----QVRIG--SSQHASGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                   PFSTS----VKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRG 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 114.5; DB 1;
Pred. No. 0.037;
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Pred. No. 0.039;
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  в.в.;
                                                                                                         human
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                                             08-Dec-2000
  Usher,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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  Flier,
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  J.S
A;Title: Primary structure of two distinct A;Reference number: A00960; MOID:82182967 A;Accession: A00960 A;Molecule type: mRNA
                                                                                 C;Accession: A00960; A20534 R;MacDonald, R.J.; Swift, G Biochemistry 21, 1453-1463,
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A; Residues: 19-44,'C',46-48
C; Comment: Factor D cleaves
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A; Residues: 1-246 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                     204
                                                                                                                                                                                                                                                                                                                                                                                          73
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                                                                                                                                                                                                                                                                                                    TLGPAVRPLPWQRV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bhown, A.S.; Ber
2482-2486, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
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pancreatic elastase (EC 3.4.21.36) I precursor -
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-198
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F;44-60,141-207,172-188,197-222/Disulfide bonds: #status predicted
F;59,105,201/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: complement alternate pathway; hydrolase; plasma; serine pre;1-18/Domain: signal sequence #status predicted <SIG>F;19-246/Product: complement factor D (fragment) #status experimental
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A;Molecule type: protein
A;Residues: 19-44,'G','46-51,'Q',53-75,'TH',78,'p',80-83,'XXXITIE',90-172,86-91,185-23
A;Residues: 19-64,'G',46-91,185-23
A;Note: a few residues were assigned from the previously published sequence of Reld e
R;Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.;
Mol. Immunol. 27, 637-644, 1990
A;Title: Molecular and functional identification and purification of complement compo
A;Reference number: A60571; MUID:90370044
A;Accession: A60571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 19-20, 'xx', 23-27, 'xx', 30-31, 'xx', 34, 'x', 36-40
R; Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
FEBS Lett. 371, 300-302, 1995
A; Title: Inhibition of degranulation of human polymorphonu
A; Reference number: S66645; MUID: 96013156
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A;Title: Human adipsin is identical to complement factor D and A;Reference number: A40197; MUID:92250520
A;Accession: A40197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 PFSTSVKLSTG--CTGTLVAEKHVLTAAHCIH---DGKTYVKGTQKLRVGFLKPKFKDGG 203
                                                                                                                                                                                                                                                                                                                                                              GVSPPAKQLPGGRIHFSGYDND-RPGNLVYRFCDV
                                                                                                                                                                                                                                                                                                                                                                                                                               LGAHSLSQPEPSKRLYDVLRA----VP----HPDSQPDTIDHDLLLLQLSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYMASVQLNGAHLCAGVLVAERWVLSAAHCLEDAADGKVQVL---
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G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits,
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Pred. No. 0.042;
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rat pancreatic preproelastases

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Biochemistry 22, 3763-3770, 1983
A/Title: Isolation and characterization of rat pancreatic elast A/Title: Isolation and characterization and characterization pancreas; A/Title: A/T
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C; Date: 24-Apr-1984 #sequence_revision 30-Sep-1990 #text_change 16-Jun-2000
C; Accession: JS0013; A26777; A10061; A00959
C; Accession: JS0013; A26777; A10061; A00959
R; Shirasu, Y: Yoshida, H: Mikayama, T.; Matsuki, S.; Tanaka, J.I.; Ikenaga, J. Biochem. 99, 1707-1712, 1986
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A; Cross-references:
R; Largman, C.
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A;Title: Three-dimensional structure of tosyl-elastase. A;Reference number: A93160; MUID:70114044
A;Reference number: A72160; MUID:70114047
A;Contents: annotation; X-ray crystallography, 3.5 angstroms; C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; serine proteinase; zymogen F;1-16/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Shotton, D.M.; Hartley, B.S.
Blochem. J. 131, 643-675, 1973
A;Title: Evidence for the amino acid sequence of
A;Reference number: A90267; MUID:73229121
A;Accession: A10061
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A; Residues: 27-91, 'N', 93-203, 'N', 205-266 <SHO>
R; Shotton, D.M. Hartley, B.S.
Nature 225, 811-816, 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA A;Fesidues: 1-125,'G',127-183,'L',185-266 <TAN> A;Residues: 1-125,'G',127-183,'L',185-266 <TAN> A;Cross-references: GB:D00160: NID:9217683; PIDN:BAA00118.1; PID:9217684 A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC A;Note: the authors translated the codon GGG for residu
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A; Residues: 1-266 <SHI>
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F;27-259/Domain: trypsin homology <TRY>F;56-72,153-220,184-200,210-240/Disulfide bonds: #status experimental F;71,119,214/Active site: His, Asp, Ser #status experimental
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c;Superfamily: trypsin; trypsin homology
c;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-32/Domain: signal sequence #status predicted <STG>
F;33-36/Domain: propeptide #status predicted <PRO>
F;35-36/Domain: propeptide #status predicted <PRO>
F;35-36/Domain: pro
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J. Mol. Biol. 200, 523, 1988
A;Title: Refined crystal structure of Streptomyces
A;Reference number: A44574; MUID:88286735
A;Contents: annotation; X-ray crystallography, 1.7
A;Note: residues 96-97 modeled as Gly-Ala
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Olafson, R.W.; Jurasek, L.; Carpenter, M.R.; Smillie, L.B. Biochemistry 14, 1168-1177, 1975
A;Title: Amino acid sequence of Streptomyces griseus trypsin. A;Reference number: A00962; MUID:75127940
A;Accession: A00962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: JQ1302; A00962
R;Kim, J.C.; Cha, S.H.; Joong, S.T.; Oh, S.K.; Byun, S.M.
Biochem. Blophys. Res. Commun. 181, 707-713, 1991
A;Title: Molecular cloning and nucleotide sequence of Streptomyces
A;Reference number: JQ1302; MUID:92095977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Streptomyces griseus
C;Date: 24-Apr-1984 #sequence_revision 12-May-1994 #text_change
C;Accession: JQ1302; A00962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                  F;37-258/Product: trypsin #status experimental <MAT>
F;37-252/Domain: trypsin homology <TRY>
F;58-74,177-192,204-233/Disulfide bonds: #status experimental
F;73,118,208/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 37-95, 98-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-259 < KIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JQ1302
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199
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208 DS---TSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIG
                                                                                                                                                       148 YPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGAN
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                                                                               FPF--MVRLSMGCGGALYAQDIVLTAAHCV
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Pred. No. 0.0
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Pred. No. 0.056;
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hypothetical protein 22592 [imported] - Escherichia coli (strain O157:H7)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: E85765
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
Pittle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
Reference number: A85480; MUID:21074935; PMID:11206551
PAccession: E85765
R;Status: preliminary
Search completed: July 12, 2001, 11:43:32 Job time: 197 sec
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A;Residues: 1-273 <STO>
A;Cross-references: GB:AE005174; NID:g12515576; PIDN:AAG56585.1; GSPDB:GN00145; UWGP:Z2:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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                                                                                                                                                                                                                                                                                                                   163 LFEGDKAALTAALKAAGRKVTQAGYPEDHLDTLYSHQNCEVTGWAQTSVMSHQCDTLPGD 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 T--LGKRLKAD------GDGWIVPPA---AAPWDFGLIVLRNPPS-----GITPLP 162
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                                                                                                                                                                                                                                                                                                                                                                       ------PAKQLPGGRIHFSGYDNDRPGNLV-YRFCDVKD-ETYDLLYQQCDAQPGA 315
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OM protein -
protein search, using sw model
                                                                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Run

July 12, 2001, 11:42:36 ; Search time 13.12 Seconds (without alignments) 999.989 Million cell updates/sec

US-09-554-933-3 2080

Title: Perfect score:

Sequence: 1 MAGIPGLLFLLFFLLCAVGQ.....LKYAQICYWIKGNYLDCREG 383

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

earched: 93435 seqs, 34255486 residues

rotal number of hits satisfying chosen parameters: 93435

Minimum DB : Maximum DB : seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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97 96.5	97.5	98.5	101.5	102	103.5	103.5	104.5	105	105	107.5	108	108	110	110	111	111	111.5	111.5	112.5	113	113	114.5	115	115.5	115.5	119	121.5	124	135.5	194	Score		
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InterPro; IPRO00126; -.
InterPro; IPR001254; -.
InterPro; IPR001254; -.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.

EMBL; D10060; BAA00949.1; -. PIR; S23078; S23078. PIR; A45134; A45134. MEROPS; S01_271; -.

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ALIGNMENTS

SULT	LT 1
1	O GSEP BACLI STANDARD: PRT: 316 AA.
12	
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-3	01-OCT-1993 (Rel. 27, Last sequence update)
3	01-NOV-1995 (Rel. 32, Last annotation update)
[-]	GLUTAMYL ENDOPEPTIDASE PRECURSOR (EC 3.4.21.19) (GLUTAMATE SPECIFIC
Į.	ENDOPEPTIDASE) (GSE).
~	BLASE.
0,2	Bacillus licheniformis.
	Bacteria; Firmicutes; Bacillus/Clostridium group;
١,,	Bacillus/Staphylococcus group; Bacillus.
^	NCBI_TaxID=1402;
~	[1]
	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
	STRAIN=ATCC 14580;
^	MEDLINE=93054737; PubMed=1429718;
	Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E.,
	Okamoto H., Shin M., Tamaki M., Teraoka H., Tsuzuki H., Yoshida N.;
_	"Purification, characterization, cloning, and expression of a
_	glutamic acid-specific protease from Bacillus licheniformis ATCC
_	14580. ";
L	J. Biol. Chem. 267:23782-23788(1992).
_	[2]
٠	SEQUENCE OF 95-316.
^	MEDLINE=92155199; PubMed=1346764;
_	
_	"Isolation and amino acid sequence of a glutamic acid specific
_	
_	Eur. J. Biochem. 204:165-171(1992).
` -	!- FUNCTION: SPECIFIC FOR HYDROLYSIS OF PEPTIDES BONDS ON THE
	CARBOXYL SIDE OF ACIDIC AMINO ACID RESIDUES, WITH A STRONG
` -	PREFERENCE FOR GLU.
` _	-!- SUBCELLULAR LOCATION: SECRETED.
. , .	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B; ALSO KNOWN AS THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=1423;
SEQUENCE OF 1-68 FROM N.A. MEDLINE-89108019; PubMed-3145906; Smith H., de Jong A., Bron S., Ve
                                                                                       "Haga K., Liu H., Yasumoto K., Takahashi H., Yo
"Sequence analysis of the 70kb region between
Bacillus subtilis chromosome.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                "Gene encoding a novel subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
EXTRACELLULAR METALLOPROTEASE PRECURSOR (EC 3
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01-FEB-1995
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EMBL; M22916; AAA22832.1; -
EMBL; M229105; CAB12018.1; -
PIR; A35122; A35122.
HSSP; P00756; 1SGF.
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B; ALSO KNOWN AS
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PRINTS; PR00722; CHYMOTRYSSIN.
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
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ACTIVATION PEPTIDE (BY SIMILARITY).

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                                                                                                                                    EMBL; AF003200; AAB62542.1;
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Mammalia; Eutheria;
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PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).

PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FINTRINSIC PATHWAY), OR BY FACTOR VIIA (IN T
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SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                                                                      MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER ANOTHER SITE, BEYOND THE GLA DOMAIN. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO
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                                                                                                                                                            opean Bioinformatics Institute. There non-profit institutions as long as d and this statement is not removed. Use requires a license agreement (See htt an email to license@isb-sib.ch).
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Lagomorpha; Leporidae; Oryctolar
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PROSITE; PSO0011; GLU_CARBOXYLATION; 1.

PROSITE; PSO0012; EGF_1; 1.

PROSITE; PSO1187; EGF_CA; 1.

PROSITE; PSO1187; EGF_CA; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Glycoprotein; Hydrolase; Serine protease; Planger of the company 
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CHARGE RELAY SYSTEM.
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BY SIMILARITY.
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Pred. No. 0.00
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EGF-LIKE 2.
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ACTIVATION PEPTIDE.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM

(BY (BY)

SIMILARITY).
SIMILARITY).

CHAIN

PROPEP

Hydrolase; SIGNAL

PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;

ne

protease;

Pancreas;

Zymogen; Signal.

PRINTS; PR00722;

Pfam; PF00089; trypsin; 1. PRINTS; PR00722; CHYMOTRYPSIN.

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01-AUG-1988 (Rel. 08, I
15-JUL-1999 (Rel. 38, I
ELASTASE 2 PRECURSOR (F
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                        EMBL; M16651; AAA31027.1;
EMBL; D00237; BAA00166.1;
PIR; A26823; A26823.
MEROPS; S01.155; -.
                                                                                                                                                                                                                                                       use by non-profit institute modified and this statement and this alicense.
                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                     Shirasu Y., Yoshida H., Matsuk
Shimada Y., Ozawa T., Mikayama
Tamai Y., Tanaka J., Ikenaga H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNAs are expressed in human DNA 6:163-172(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of pancreatic elastase mRNAs are expressed in human pancreas.";
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                                                                                                                                                                                                                                           entities requires a or send an email to
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-!- TISSUE SPECIFICITY: PANCREAS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
TRYPSIN FAMILY. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                        encoding human pancreatic elastase J. Biochem. 102:1555-1563(1987).
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-!- CATALYTIC ACTIVITY: PREFERENTIAL CAND PHE-|-XAA. HYDROLYSES ELASTIN
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j; PubMed=2834346;

hida H., Matsuki S., '

havama T., J
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DT ELASTA
OS Homo s
OC EUKARY
OC Mammal
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RN 161
RT SEQUEN
RX MEDLIN
RA KAWAS
RT BLAAS
BT MRNAS
DNA 6:
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Best Local
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Fletcher T.S., Shen W.F., Largman C.;
*Primary structure of human pancreatic elastase 2 determined b
sequence analysis of the cloned mrNA.";
Blochemistry 26:7256-7261(1987).
-!- FUNCTION: ACTS UPON ELASTIN.
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: LEU-|-XAA, MET-
AND PHE-|-XAA. HYDROLYSES: ELASTIN.
-!- SUBCELJULAR LOCATION: SECRETED.
-!- TISSUE SPECIFICITY: PANCREAS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
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01-AUG-1988
01-OCT-2000
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SEQUENCE
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01-OCT-2000 (Rel. 40, Last annotation update)
ELASTASE 2A PRECURSOR (EC 3.4.21.71).
                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   *Rawashima I., Tani T., Shimoda K., Takigu

"Characterization of pancreatic elastase

"RNAs are expressed in human pancreas.";

DNA 6:163-172(1987).
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                                                                                                             the
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                            European
                                                                                                                                                                   TRYPSIN FAMILY. ELASTASE SUBFAMILY.
                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLSNGNDIALLKLASPVSLTDKIQLGCLPAAGTILPNNYVCYVTGWGREQTNGASPDILQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TY--VKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAN 239
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           M16631; AAA52374.1;
M16652; AAA52380.1;
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S -> Y (IN REF. 2).
I -> V (IN REF. 2).
C -> V (IN REF. 2).
BAC6FE69AF4DDE56 CRC64;
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astase II cDNAs: two
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                                                                                             There are no restrictions ng as its content is in
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InterPro; IPR001314; -.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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13-AUG-1987 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
SIGNAL
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MEROPS; S01.155; -.
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                                                   TRYPSIN FAMILY. ELASTASE
                                                                  TISSUE SPECIFICITY: PANCREAS.
SIMILARITY: BELONGS TO PEPTIDASE
                                                                                                                                                                                                          musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                            DGGRG----ANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP- 255
                                                                                                                                                                                                                                                                                                                                HKRKFMKIGVSPPAKQ-LPG------GRIHFSGYDND--RPGNLV---YRFC
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Last annotation updat
(EC 3.4.21.71).
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                                                           SUBFAMILY.
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                                                                   FAMILY S1;
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                                                                                                     LEU-|-XAA,
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European Bioinformatics Institute.

non-profit institutions as long as its content and this statement is not removed "----

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Matches 67
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EMBL; X04576; CAA28244
PIR; A25528; A25528.
MEROPS; S01.155; -.
MGD; MGI:95316; Ela2.
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                                                                                      981428;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
COAGULATION FACTOR X (EC 3.4.21.6) (TROCARIN PROTHROMBIN ACTIVATOR
Tropidechis carinatus (Australian rough-scaled snake).
Tropidechis carinatus (Australian rough-scaled snake).
Tropidechis carinatus (Australian rough-scaled snake).
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InterPro; IPR001314; -.
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P81428;
                   MEDLINE-99326314; PubMed-10397729;
Joseph J.S., Chung M.C.M., Jeyaseelan K., Kini R.M.;
"Amino acid sequence of trocarin, a prothrombin activator
                                                          SEQUENCE, AND CHARACTERIZATION
                                                                             NCBI_TaxID=100989;
                                                                                                                                                                                                                               248
 Tropidechis carinatus venom: its structural similarity factor Xa.";
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                                                                                                                                                                                                                                                                                                            KNIQTACLPPAGTILPRNYVCYVTGWGLLQTNGNSPDTLRQGRLLVVDYATCSSASWWGS
                                                                                                                                                                                                                                                                                                                          KFMKIGVSPPAKQ-LPGGRI-HFSGY------DNDRPGNLV---YRFC-----
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CAA28244.1;
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Gamma-carboxyglutamic acid;
Zymogen; EGF-like domain; R
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PROSITE; PS00021; GLU_CARBOXYLATION;
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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              DISULFID
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                                                                                  DISULFID
                                                                                                                                                                                                                                                                    MOD_RES
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CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-|-THR AND THEN ARG-|-TLE BONDS IN PROTHROMBIN TO FORM THROMBIN.

ARG-|-TLE BONDS IN PROTHROMBIN TO FORM A SINGLE-CHAIN PRECURSOR SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR AND ARE HELD TOOSTHER BY 1 OR MORE DISULFIDE BONDS.

AND ARE HELD TOOSTHER BY 1 OR MORE DISULFIDE BONDS.

PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.

CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA. CALCIUM, AND PHOSPHOLIPID DURING BLOOD CLOTTING. ACTS AS A TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTRINSIC PATHWAY), OR SIMILARITY: CONTAINS 2 SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN TINTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PASIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d; Hydroxylation;
Repeat.
FACTOR X LIGH?
                GAMMA-CARBOXYGLUTAMIC A
HYDROXYLATION (BY SIMIL
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATED FACTOR XA, HEAVY (
EGF-LIKE 1, CALCIUM-BINDING
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X LIGHT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X HEAVY CHAIN.
                                                                                                                                                                                  MYGLUTAMIC ACID.

BOXYGLUTAMIC ACID.

BOXYGLUTAMIC ACID.

VOXYGLUTAMIC ACID.

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; Calcium-binding; Vitamin
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01-APR-1993 (Rel. 2
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Hydrolase;
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SEQUENCE FROM N.A.
MEDLINE-97242546; PubMed-9087545;
MEDLINE-97242546; Prosser D.E.,
                                                         InterPro; IPR001254; -.
Pfam; PF00089; trypsin; 1.
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
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PIR; S19891; TRWV5Y.
HSSP; P00763; 1DPO.
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Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
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SEQUENCE
                                                                                                                                                                                                                                                       entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for trypsin-like enzymes from the mi
Insect Mol. Biol. 2:71-79(1993).
-!- FUNCTION: MAJOR FUNCTION MAY BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Culicidae; Aedes.
NCBI_TaxID=7159;
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01-CCT-1996 (Rel. 34, Last annotation update)
TRYPSIN 5G1 PRECURSOR EC 3.4.21.4) (FRAGMENT).
                                                                                                                                                                                                                                                                                                modified and
                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: MIDGUT.
SIMILARITY: BELONGS TO PEPTIDASE
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                                       Digestion; Multigene family.
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Aedes a
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P00772; Q29625;
21-JUL-1986 (Rel. 0
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15-JUL-1999 (Rel. 3
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                                   MEDLINE=70114042; PubMed=5415108
Shotton D.M., Hartley B.S.;
"Amino-acid sequence of porcine
homologies with other serine pro
                                                                                                                          MEDLINE-73229121; Pubw
shotton D.M., Hartley
                                                                                                                                                                 Tani T., Kawashima I., Furukawa H., Ohmine T. "Characterization of a silent gene for human structure of the 5'-flanking region.";
J. Biochem. 101:591-599(1987).
                                                                                                                                                                                                MEDLINE-87250343; PubMed-3648024; Tani T., Kawashima I., Furukawa H
                                                                                                                                                                                                                                      "Isolation and expression in Escherichia encoding porcine pancreatic elastase.";
J. Biochem. 99:1707-1712(1986).
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-86304235; Poshida
Shirasu Y., Yoshida
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria;
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MEDLINE=78111463;
         X-RAY CRYSTALLOGRAPHY
                             Nature
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l Similarity 29.4%;
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da H., Mikayama
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"The atomic structure of crystalline porcine pancreatic elastase at 2.5-A resolution: comparisons with the structure of alpha-chymotrypsin.";
alpha-chymotrypsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95006335; PubMed-7922044; Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.; "The molecular structure of the complex of Ascaris chymotrypsin/elastase inhibitor with porcine elastase."; structure 2:679-689(1994).
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Shotton D.M., Watson H.C.;
"Three-dimensional structure of tosyl-elastase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - FUNCTION: ACTS UPON ELASTIN.
- ACTAVITY: HYDROLYSIS OF PROTEINS,
- PREFERENTIAL CLEAVAGE: ALA-[-XAA.
- SUBCELLULAR LOCATION: SECRETED.
- TISSUE SPECIFICITY: PANCREAS.
- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1;
- TRYPSIN FAMILY.
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                       1BOE; 18
1BTU; 16
PS; SO1.1
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30-APR-94.
15-OCT-92.
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07-FEB-95.
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27-JAN-97.
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Query Match 5.4%; Score 113; DB 1; Best Local Similarity 27.3%; Pred. No. 0.022; Matches 36; Conservative 21; Mismatches 41

41;

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Gaps

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Length 266; Indels

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                                                                                                                                                                                                                                                                                                                                                 Swift G.H., Craik C.S., S
Rutter W.J., Macdonald R.
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"Primary structure of two distinct determined by sequence analysis of ribonucleic acid sequences.";
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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MEDLINE-82182967; PubMed=6918221;
-14 p. T. Swift G.H., Quinto
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01-FEB-1994
01-NOV-1995
                                                                   MEDLINE-92095977; PubMed-1755852;
Kim J.C., Cha S.H., Jeong S.T., Oh
"Molecular cloning and nucleotide s
trypsin gene.";
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PIR; A00960; E
HSSP; P00772;
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Olafson R.W., Jurasek L., Carpenter M.R., Smillle L.B.;
"Amino acid sequence of Streptomyces griseus trypsin. Cyanogen
bromide fragments and complete sequence.";
Biochemistry 14:1168-1177(1975).
                                   SEQUENCE OF 37-259.
MEDLINE-75127940; P
                                                                                                                                                       Streptomyces griseus.
Bacteria; Firmicutes;
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Pfam; PF00089; trypsin;
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DR PETER TERMENT
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X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE-88286735; PubMed=3135412;
Read R.J., James M.N.G.;
Read R.J., James M.N.G.;
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PIR; JQ1302; JQ1302.
PDB; 1SGT; 16-JUL-88.
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MEDIJINE-91216473; PubMed=1902434;
MESSier T.L., Pittman D.D., Long G.L.,
"Cloning and expression in COS-1 cells
human coagulation factor X.";
Gene 99:291-294(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
Gene 41:311-314(1986).
[5]
SEQUENCE OF 41-179.
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Mammalia; Eutheria;
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                                                                                                         MEDLINE=86221713; PubMed=3011603; Kaul R.K., Hildebrand B., Roberts
                                                                                                                                                                                                                 Fung M.R., Hay C.W., McGillivray R.T.A.;
"Characterization of an almost full-length cDNA coding blood coagulation factor X.";
proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
                                                                                                                                                                                                                                                                                                SEQUENCE OF 13-488 FROM N.A. MEDLINE=85216545; PubMed=2582420;
                                                                                                                                                                                                                                                                                                                                                                                                      Leytus S.P., Foster D.C., Kurachi K., Davie E.W.; "Gene for human factor X\colon a blood coagulation factor whose gene organization is essentially identical with that of factor IX and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-87026600; PubMed=3768336;
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                                                                                        "Isolation
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                                                                                     \label{eq:hildebrand B., Roberts S., Jagadeeswaran P.; and characterization of human blood-coagulation \\
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Kwa E.Y., Weinstein P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 183-234,
MEDLINE-94062825; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-hydroxyaspartic acid.";
Biochemistry 22:2875-2884(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete amino acid sequence of the light chain of human blood coagulation factor X: evidence for identification of residue 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural
factor Xa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kamata K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98283982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inoue K., Morita T.;
                                                                                                                                                                                                                                                                                                                                                                                                     TOT MA.";

CON MAIL. ACAD. SCI. U.S.A. 95:6630-6635(1998).

CUNCTION: FACTOR XA IS A VITAMIN K-DEPENDENT GLYCOPROTEIN THAT CONVERTS PROTHROMBIN TO THROMBIN IN THE PRESENCE OF FACTOR VA, CONVERTS PROTHROSPHOLIPID DURING BLOOD CLOTTING. CA++, AND PHOSPHOLIPID DURING BLOOD CLOTTING. CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-1-THR AND THEN ARG-1-ILE BONDS IN PROTHROMBIN TO FORM THROMBIN.

SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                                                             MORE DISULFIDE BONDS:
PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO B CALCIUM.
PTM: N- AND O-GLYCOSYLATED.
PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (I INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN TRYPSIN FAMILY.
            K03194; AAA52490.1;
M57285; AAA52764.1;
L29433; AAA52764.1;
L00390; AAA52764.1;
L00391; AAA52764.1;
L00392; AAA52764.1;
L00393; AAA52764.1;
L00394; AAA52764.1;
L00394; AAA52764.1;
L00396; AAA52764.1;
L00396; AAA52764.1;
L00396; AAA52764.1;
L00396; AAA52764.1;
L00396; AAA52764.1;
                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  basis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed-9618463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8355279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34, AND CARBOHYDRATE-LINKAGE SITES PubMed=8243461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Η.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human blood coagulation
                                                                                                                                                                                                                                                                                                                   FACTOR IXA (IN THE THE EXTRINSIC PATHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND
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  PRINTS; PRO0001; GLABLOOD.

PRINTS; PRO0722; CHYMOTRYPSIN.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00011; GLL_CARBOXYLATION; 1.

PROSITE; PS00012; EGF_1; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS01187; EGF_CA; 1.
DISÜLFID
DISULFID
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ACT_SITE
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CARBOHYD
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pfam; PF00594; gla; 1.
pfam; PF00089; trypsin;
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InterPro; IPR001881;
InterPro; IPR002383;
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CarbBank; CCS
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A24478; A24478.

1HCG; 08-MAY-95.

1FAX; 29-OCT-97.

1FXY; 17-JUN-98.

1XKA; 23-MAR-99.
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; IPR000561;
; IPR001254;
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 P00742;
D:29393;
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                          GAMMA CARBOXYGLUTAMIC A
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                                                                                                                                             N-LINKED
N-LINKED
CHARGE RE
CHARGE RE
                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1.
CATALYTIC.
CATALYTIC.
                                                     INTERCHAIN
                                                                                                                                                                                                                                       HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat;
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X HEAVY CHAIN.
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This

EMBL; EMBL;

SQ

CONFLICT CONFLICT SEQUENCE

285 442 488

288 K 442 G 54731 MW;

KVRV -> E (IN REF. 4 AND G -> S (IN REF. 3).; F81D5746AF4797AF CRC64;

<u>6</u>

AA;

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RESULT 14
NETR_HUMAN
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Best Local Similarity
Matches 49; Conserv
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30-MAY-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                      InterPro;
InterPro;
                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                  + +
                                                                                                                                                                                                                                                                                                                                             Proba K., Gschwend T.P., Sonderegger P.;
"Cloning and sequencing of the cDNA encoding human neurotrypsin.";
Biochim. Biophys. Acta 1396:143-147(198).
-i- FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLY
ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH
LEARNING AND MEMORY OPERATIONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEUROTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P56730;
PRINTS; PR00258; SPERACTRCPTR.
PRINTS; PR00722; CHYMOTRYESIN.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00420; SPERACT_RECEPTOR;
                                                                                                                             EMBL; AJ001531; CAA04816.1;
                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98201705; PubMed=9540828;
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                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270
                                                                                                 InterPro;
                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 KRINGLE DOMAIN. SIMILARITY: CONTAINS 4 SRCR DOMAINS.
                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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IPR001314;
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(Rel.
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(Rel. 40, Last annotation update)
PRECURSOR (EC 3.4.21.-) (MOTOPSIN).
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TO PEPTIDASE FAMILY
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Pred. No. 0.06;
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
white R.T., Damb D., Hancock N., Rosen B.S Flier J.S., Spiegelman B.M.; "Human adipsin is identical to complement at high levels in adipose tissue."; J. Biol. Chem. 267:9210-9213(1992). [2]
                                                                                                                                          P00746;
21-JUL-1986 (Rel. 01, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
COMPLEMENT FACTOR D PRECURSOR (EC 3.4.21.46) (C3 CONVERTASE ACTIVATOR)
(PROPERDIN FACTOR D) (ADIPSIN).
                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                            SEQUENCE OF 8-253 FROM N.A. MEDLINE=92250520; PubMed=1374388;
                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                      CFAD_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                     --CTGTLVAEKHVLTAAHCIHDGKTYVKGTQK--LRVGFLKPKFKDGGRGANDSTSAMPE 215
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SRCR 2.
SRCR 3.
SRCR 4.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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CHARGE RELAY SYSTEM.
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Pred. No. 0.12;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94118317; PubMed-8289289;
Narayana S.V.L., Carson M., El-Kabbani O., K
Chen X., Bugg C.E., Volanakis J.E., Delucas:
"Structure of human factor D. A complement s;
resolution.";
J. Mol. Biol. 235:695-708(1994).
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Niemann M.A., Bhown A.S., Bennett J.C., Volanakis J.E.;
*Amino acid sequence of human D of the alternative complement pathway.";
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Flier J.S., Spiegelman B
Patent number WO9006365,
[3]
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*Practor D of the alternative pathway of human complement.

*Purification, alignment and N-terminal amino acid sequences of the major cyanogen bromide fragments, and localization of the serine
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                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enhanced catalytic activity."
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Davis A.E. III;
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Proc. Natl.
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residue at the active site.";
Biochem. J. 187:863-874(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Crystal structure of a complement factor D mutant expressing
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Kim S., Narayana S.V., Volanakis
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Volanakis J.E., Bhown A.S., Benne
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Johnson D.M.A., Gagnon
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MEDLINE-84108950; PubMed-6
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                                                                                                                                                                                                                                                 TRYPSIN FAMILY.

CAUTION: IN ADDITION TO THE CONFLICTS SHOWN IN THE FEATURE TABLE, REF. 3 SEQUENCE HAD A PEPTIDE IN THE WRONG ORDER AND ANOTHER ONE
                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 270:24399-24405(1995).

FUNCTION: FACTOR D CLEAVES FACTOR B WHEN THE LATTER IS COMPI WITH FACTOR C3B, ACTIVATING THE C3BBB COMPLEX, WHICH THEN BITHE C3 CONVERTASE OF THE ALTERNATE PATHWAY. ITS FUNCTION IS HOMOLOGOUS TO THAT OF C1S IN THE CLASSICAL PATHWAY.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE CASSICAL PATHWAY.
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n D.M.A., Gagnon J., Reid K.B.M.;
acid sequence of human factor D
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Gapop 10.0 , Gapext 0.5
   425026 seqs, 132305027 residues
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sp_bacteria:*
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sp_vertebrate:*
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O9qx85 rattus norv
O9qx90 rattus norv
O9qx90 rattus norv
O9qx84 rattus norv
O9qx84 rattus norv
O9qx61 ctenocephal
O9qdu8 drosophila
O6qqqq
                                                                                                                                       O95084 homo sapien
Q9exr9 bacillus in
Q9exr9 bacillus in
Q9md9 ornithorhyn
Q9nat0 anopheles g
Q9jjs8 rattus norv
Q9njs5 anopheles g
Q46644 macaca fasc
          Q9vqr8 drosophila
Q9w5u8 drosophila
O01771 caenorhabdi
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\$ \$01.309; \$ \$01.309; \$ \$0.309; \$ \$10.001 \$ \$1	TISSUE-UTENUS; Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY!- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1). EMBL; AF015287; AAD01553.1; EMBL; AF193611; AAF07186.1; EMBL; AL136914; CAB66848.1;	Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. [2] [2] SEQUENCE FROM N.A. Sheppard P., Blumberg H., Jelinek L., Foster D., O'Hara P.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. [3] [3] [3] SEQUENCE FROM N.A.	NCBI_TAXID=9606; [1] SEQUENCE FROM N.A. TISSUE=UMBILICAL VEIN; Li X., Tedder T.F.; "A novel serine protease from human umbilical vein endothelial cells ".	NARY; PRT; 383 AA. rel. 10, Created) rel. 10, Last sequence update) rel. 16, Last annotation update) POTHETICAL 43.0 KDA PROTEIN). Ontodata; Craniata; Vertebrata; Designator. Catarrhini. Hominidae.

homo sapien

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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus intermedius.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1400;
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                                      IAPNKILTNGHCVYNTASRSYSAKGS------VYP-----GMNDSTAVNGS-----
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Pred. No. 2e-181;
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Pred. No. 0.00088;
0; Mismatches 98
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ridentification and structural analysis of three serine monotreme, platypus, ornithorhynchus anatinus.";

submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF275654; AA600453.1;

SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ornithorhynchus anatinus (Duckbill platypus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
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01-MAR-2001
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01-MAR-2001
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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Pterygota; Neoptera;
Anopheles.
NCBI_TaxID=7165;
                       Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
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                                                           SP22D
                                                                        ADHESIVE SERINE PROTEASE
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|----IVGVHNAGYSNGTINGGPK 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2%; ilarity 26.5%; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                  460
                                                                                                                                                                                                                                                                                                                                             ------DFDIAVIKLKTPIT---FRMNVSPACLPEKDWAEDI 349
                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 129; DB 6; I
Pred. No. 0.0018;
0; Mismatches 73;
                                                                                      Last sequence update)
Last annotation update)
                                                                                                                Created)
                                                                                                                                         1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469
                            Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                         A
                                        Hexapoda; Insecta;
                               Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                               Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  08;
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RESULT
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Best Local
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                                                     Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Rodent
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR00268; SPERACTRCPTR.
PROSITE; PS00269; LDLRA_1; 1.
PROSITE; PS50068; LDLRA_2; 2.
PROSITE; PS500420; SRCR_1; UNKNOW!
PROSITE; PS500437; SRCR_2; 2.
PROSITE; PS500134; TRYPSIN_SER; 1
PROSITE; PS00135; TRYPSIN_SER; 1
                                                                                                                                                                                                                                                                                                                        Q9JJS8;
Q9JJS8;
                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MANNOSE-BINDING PROTEIN ASSOCIATED SERINE PROTEASE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00057; ldl_recept_a; 2. Pfam; PF00089; trypsin; 1. Pfam; PF00530; SRCR; 2. Pfam; PF01607; Chitin_bind_2; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
EMBL; AJ276428; CAB81934.1; -.
InterPro; IPR001190; -.
InterPro; IPR001124; -.
InterPro; IPR001114; -.
                                                                                                                                                                           MASP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00494; ChtBD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A modular chitin-binding
hemolymph in the mosquito
Proc. Natl. Acad. Sci. U.S
  SEQUENCE FROM N.A.
Wallis R., Dodd R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE-20318993; PubMed-10860981;
                                                                                                                                                                                                  (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danielli A., Loukeris
Kafatos F.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LDLRA) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVVHGSE---TVYG-----HPWQASLRLKTMHWCGAVLITRYHVLTAAHCLIG---YPK 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멀=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIAVVVLKTPVRFNDYVQPICLPARDAPYLPGQNCTISGWGATEAGS------KDSSY 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYALLELKKPHKRKFMKIGVSPPAKQ---LPGGRIHFSGYDNDRPGNLVYRFCDVKDETY 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STYRVRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQIYGYDSRFSIFGKDFLLNYPFSTSVKLST--GCTGTLVAEKHVLTAAHCIHDGKTYVK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
46; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1221
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                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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SRCR_2; 2.
TRYPSIN_HIS; UNKNOWN_1.
TRYPSIN_SER; 1.
                                                                                                 Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DYHTAAYDNAELD-IFIENTYIHEQFREGH----HMSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ως;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 127.5; DB 5;
Pred. No. 0.0097;
5; Mismatches 58;
                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ν
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                                                                                                   Rattus
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RESULT
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PROSITE; PS00010; ASX_HYDROXYL; U
PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                  Q9NJS5;
Q1-OCT-2000
Q1-OCT-2000
Q1-OCT-2000
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000152; -.
InterPro; IPR000436; -.
InterPro; IPR000561; -.
InterPro; IPR000859; -.
InterPro; IPR001859; -.
InterPro; IPR001154; -.
InterPro; IPR001184; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
NON_TER
SIGNAL
Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SP22D.
                                                       01-OCT-2000 (TremBLrel.
01-OCT-2000 (TremBLrel.
01-MAR-2001 (TremBLrel.
SERINE PROTEASE 22D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00084; sushi; 2. Pfam; PF00089; trypsin; 1. Pfam; PF00431; CUB; 2.
                                                                                                                Q9NJS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calcium-binding; EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00032; CCP;
                                                                                                                                                                                                                                                                                                         466
                                                                                                                                                                      614
                                                                                                                                                                                           316
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                                                                                                                                                                     DAGGKDSCRGDSGGALVFLDNETQRW--FVGGIVS---WGSINCGGSEQYGVYTKVT
                                                                                                                                                                                                                                                                                                                                                                           RDS-
                                                                                                                                                                                                                V--AGWGLTQKGFLARNLMFVDIPIVD
                                                                                                                                                                                                                                                                                                        HDDWVLTAAHAVY-GKTEAMSSLDIRMGILK-----
                                                                                                                                                                                                                                                                                                                                                                                                CGPPDDLPNGHVDYITGPEVTTYKAVIQYSCEETFYTMSSN-----GKYVCEADGFWTSS 413
                                                                                                                                                                                                                                      IHFSGYDNDRPG----NLVYRFCDVKDETYDLLYQQC-----DAQPGA------
                                                                                                                                                                                                                                                                                  RTHVPKGWIKGNANDIGMDYDYALLELKK--PHKRKFMKIGVSPPAKQLPG-----
                                                                                                                                                                                                                                                                                                                             AEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVK 225
                                                                                                                                                                                         -----SGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMN-GSPQDFNVAVRIT
                                                                                                                                                                                                                                                             --FIHEGYTHG----AGFDNDIALIKLKNKVTINRNIMPICL--PRKEAASLMKTDFVGT 561
                                                                                                                                                                                                                                                                                                                                                     KGEKSLPVCKPVCGLSTHTSGGRIIGGQPAKPG-----DFPWQVLLLGETTAAGALI 465
                                                                                                                                                                                                                                                                                                                                                                                                                                           79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    678
                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                        -GSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
12
678
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                                                                 15,
16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                 Last sequence update)
Last annotation update)
                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 126.5;
Pred. No. 0.00
6; Mismatches
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MANNOSE-BINDING
PROTEASE-2.
                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNKNOWN_1.
            Diptera;
                                                                                                                                                                                                                 HQKCATAYTKQPYPGAKVTVNMLCAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0049;
                       Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                         RLSPHYTQAWPEAV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                            123;
            Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN ASSOCIATED SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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            Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat;
                                                                                                                                                                       665
                                                                                                                                                                                                                                                                                   GR 276
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C (ILLRA) DOMAIN.

C (ILLRA) DOMAIN.

C (I SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

C (I SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

C (I SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

C (I SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

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C (I SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

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C (I SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

C (I SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

C (I SIMILARITY: TO CHYMOTRYPSIN SERI
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Best Local S
Matches 45
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PRINTS; PRO07261; LDLRECEPTOR.
PRINTS; PRO0261; LDLRACTRCTPR.
PRINTS; PRO0256; SPERACTRCTPR.
PROSITE; PSO1209; LDLRA_1; 1.
PROSITE; PSO9068; LDLRA_2; 2.
PROSITE; PSO90420; SRCR. 1; UNKNOWN_1.
PROSITE; PSO90134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PSO90134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PSO90135; TRYPSIN_SER; 1.
SMART; SM00494; ChtBD2; 1.
                                                                                                                                                                                                    O46644;
O46644;
O1-JUN-1998 (TrEMBLrel. 06, C
O1-JUN-1998 (TrEMBLrel. 06, I
O1-MAR-2001 (TrEMBLrel. 16, I
ELASTASE I PRECURSOR.
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Gorman M.J., Andreeva O.V., Paskewitz S.M.;
Gorman M.J., Andreeva O.V., Paskewitz S.M.;
Molecular characterization of five serine protease genes cloned f
"Molecular characterization of five serine protease genes cloned f
anopheles gambiae hemolymph.";
Insect Biochem. Mol. Biol. 30:35-46(2000).
-i- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1078
                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Cercopithecinae; Macaca.
NCBL_TaxID-9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1220 DL
                                                                                                                                                  Macaca fascicularis
     SEQUENCE FROM N.A.
                                                                                                                                                                                  ELA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIAVVVLKTPVRFNDYVQPICLPARDAPYLPGQNCTISGWGATEAGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYALLELKKPHKRKFMKIGVSPPAKQ---LPGGRIHFSGYDNDRPGNLVYRFCDVKDETY 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVVHGSE---TVYG-----HHPWQASLRVKTMHWCGAVLITRYHVLTAAHCLIG---YPK 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQIYGYDSRFSIFGKDFLLNYPFSTSVKLST--GCTGTLVAEKHVLTAAHÇIHDGKTYVK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STYRVRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1322 AA; 146811 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%;
                                                                                                                               (Crab eating macaque) (Cynomolgus monkey).
Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DYHTAAYDNAELD-IFIENTYIHEQFREGH----HMSN 1167
                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Pred. No. 0.018;
                                                                                                             Catarrhini;
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                               266
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                                                                                                             Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDSSY 1219
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RA REL CCC CCC CCC CCC DR DR DR DR DR DR DR DR DR TT TW
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Best Local S
Matches 36
Query Match
Best Local Similarity
                                                                                                                          pfam; pF00084; sushi; 1.
pfam; pF00089; trypsin; 1.
pRINTS; PR00722; CHYMOTRYPSIN.
pROSITE; pS00135; TRYPSIN_SER:
SMART: SMOOO?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
-!- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
EMBL; X91400; CAA62746.1;
HSSP; P00772; 1ELG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9QX91
Q9QX91;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001314; -. pfam; pF00089; trypsin; 1. pRINTS; pR00722; CHYMOTRYPSIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER; SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001254; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASP-2 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-FISHER 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MASP-2.
                                                                                                                                                                                                                          InterPro; IPR000436; InterPro; IPR001254; InterPro; IPR001314; InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWPSQISLOYLSGGSWYHTCGGTLIRQNWVMTAAHCVDSPKTF-----RVVVVG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVQLGVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHNLSQNDGTE - - - - -
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36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, ) (TrEMBLrel. 13, l (TrEMBLrel. 16,
                                                                                     339
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                                                                                     A,
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                                                                                                                                                 TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.0%;
                                                                                       36950 MW;
        5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QYVSVQKIVVHPYW---NSNNVAAGYDIALLRLAQSVTLNS 133
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POTENTIAL.

POTENTIAL.

POTENTIAL.

W; 6B3281B90F53A91C CRC64;
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Last annotation updat
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Pred. No. 0
        Score 123.5; DB pred. No. 0.0036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN_1
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                                DB 11;
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                                  Length
                                      339;
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RESULT
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Best Local
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                                                                                                                                            NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                        Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00135; TRYPSIN_SER;
SMART; SM00032; CCP; 1.
                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                    InterPro; IPR000436; -.
InterPro; IPR001254; -.
InterPro; IPR001314; -.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-FISHER 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9QX85
                                                                                                                                                                                                                                                       EMBL; Y18571; CAB65388.1;
HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                             MAP1
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 102
                      116
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                                                                                                                                                                                                                                                                                                                                                                                                                         MAY-2000 (TrEMBLrel.
MAR-2001 (TrEMBLrel.
19 PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                       RDS
                                                                  CGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRGGKDSCRGDSGGALVFLDNETQRW--FVGGIVS---WGSINCGGSEQYGVYTKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V--AGWGLTQKGFLARNLMFVDIPIVD-----HQKCATAYTKQPYPGAKVTVNMLCAGL
 KGEKSLPVCKPVCGLSTHTSGGRIIGGQPAKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --FIHEGYTHG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HDDWVLTAAHAVY-GKTEAMSSLDIRMGILK-----RLSLIYTQAWPEAV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGP----
                                          CGPPDDLPNGHVDYITGPEVTTYKAVIQYSCEETFYTMSSN-----GKYVCEADGFWTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IHFSGYDNDRPG----NLVYRFCDVKDETYDLLYQQC-----DAQPGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTHVPKGWIKGNANDIGMDYDYALLELKK--PHKRKFMKIGVSPPAKQLPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGEKSLPVCKPVCGLSTHTSGGRIIGGQPAKPG-----DFPWQVLLLGETTAAGALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGPPDDLPNGHVDYITGPEVTTYKAVIQYSCEETFYTMSSN-----GKYVCEADGFWTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79;
                                                                                     Similarity 22.79; Conservative
                                                                                                                                           366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMN-GSPQDFNVAVRIT
                                                        -QCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQH 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·QCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQH 115
                                                                                                                                                                           TRYPSIN_SER;
                    GSSGKSRKKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AGFDNDIALIKLKNKVTINRNIMPICL--PRKEAASLMKTDFVGT 222
                                                                                                                                            39882 MW;
                                                                                               5.9%;
22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    13,
13,
                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                Score 123.5; DE Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                            F84F5ACF0EC93468 CRC64;
                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366
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                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                          DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123;
                                                                                                                                                                                                                                                                                                                                                                               Muridae;
                                                                                       123;
DFPWQVLLLGETTAAGALI
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                             components
                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomí;
                                                                                                                                                                                                                                                                                                                                                                               Murinae;
                                                                                     109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                               Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
153
                                          101
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                                                                                     19;
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RESULT
Q9QX90
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                                                                                               Query Match
Best Local S
Matches 79
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Q9QX90;
01-MAY-2000
                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                             Interpro; IPR001314; -.
pfam; pF00084; sushi; 2.
pfam; pF00089; trypsin; 1.
pfam; pF00431; CUB; 1.
pRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                            PROSITE; PS00010; ASX_HYDROXYL;
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00135; TRYPSIN_SER; 1
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y18566; CAB65383.1; HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                              Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.; "The Rat and mouse homologues of MASP-2 and MAp19, compoundan-Binding Lectin Activation Pathway of Complement." Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=FISHER 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (1
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TREMBLIEL 13, 01-MAY-2000 (TREMBLIEL 13, 01-MAR-2001 (TREMBLIEL 16,
                                                                                                                                                                                    EGF-like domain;
                                                                                                                                                                                                   SMART; SM00032; CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MASP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASP-2 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                            InterPro; IPR000859; -.
InterPro; IPR001254; -.
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000436; -. InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000152; -.
277
                         116
                                                                                                                                                                                                                                                                                                                                                                                                                      ·!- SIMILARITY:
                                                  222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302
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                                                                         CGP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRGGKDSCRGDSGGALVFLDNETQRW---FVGGIVS---WGSINCGGSEQYGVYTKVT
                         RDS--
                                                  CGPPDDLPNGHVDYITGPEVTTYKAVIQYSCEETFYTMSSN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V--AGWGLTQKGFLARNLMFVDIPIVD------HQKCATAYTKQPYPGAKVTVNMLCAGL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGEKSLPVCKPVCGLSTHTSGGRIIGGQPAKPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HDDWVLTAAHAVY-GKTEAMSSLDIRMGILK-----RLSLIYTQAWPEAV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHFSGYDNDRPG----NLVYRFCDVKDETYDLLYQQC-----DAQPGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --FIHEGYTHG----AGFDNDIALIKLKNKYTINRNIMPICL--PRKEAASLMKTDFVGT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTHVPKGWIKGNANDIGMDYDYALLELKK--PHKRKFMKIGVSPPAKQLPG-----
                                                                                                 1 Similarity 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMN-GSPQDFNVAVRIT
                                                                                                                                                              541
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
                                                                    -QCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQH
                                                                                                                                                                                    Glycoprotein
                      -GSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rat).
a; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodentia;
                                                                                                                                                              59323 MW;
                                                                                                             5.9%;
22.1%;
                                                                                                 46;
                                                                                               Score 123.5;
Pred. No. 0.00
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                              51EBC0C1A8549CA8
                                                                                                                                                                                                                                                    UNKNOWN_1.
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                                                                                                                        DB 11;
                                                                                                 123;
-DFPWQVLLLGETTAAGALI
                                                                                                                                                              CRC64
                                                                                                 Indels
                                                  -GKYVCEADGFWTSS 276
                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           components
                                                                                                 109;
                                                                                                                         541;
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                                                                                                Gaps
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                                                                        115
328
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RESULT
Q9JJP3
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                                                                                                                                                               SQ SQ
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                    δÃ
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밁
                                                                                                 Query Match
Best Local S
Matches 79
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20054576; PubMed-10586086; Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.; Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.; The rat and mouse homologues of MASP-2 and MAP19, components mannan-binding lectin activation pathway of complement."; J. Immunol. 163:6848-6859(1999).
J. IMMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASP-2 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9JJP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              д9ллрз;
                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-FISHER 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329
                                                                                                                                                                                                                 PRINTS: PRO0722; CHYMOTRYPSIN.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166
                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000152; -.
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                        Calcium-binding;
                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                 [nterPro;
                                                304 CGPPDDLPNGHVDYITGPEVTTYKAVIQYSCEETFYTMSSN---
  359
                         116
                                                                           65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMN-GSPQDFNVAVRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V--AGWGLTQKGFLARNLMFVDIPIVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IHFSGYDNDRPG----NLVYRFCDVKDETYDLLYQQC-----DAQPGA------ 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FIHEGYTHG----AGFDNDIALIKLKNKVTINRNIMPICL--PRKEAASLMKTDFVGT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTHVPKGWIKGNANDIGMDYDYALLELKK--PHKRKFMKIGVSPPAKQLPG---
                                                                                                                                                                                                                                                                                          erPro; IPR001254; ...
erPro; IPR001314; ...
erPro; IPR001881; ...
erpr00084; sushi; 2...
erpr00089; trypsin; 1.
erpr00431; CUB; 1.
                                                                           CGP---
                                                                                                                                                                                                                                                                                                                                                                                                                         Y18564; CAB70973.1;
  KGEKSLPVCKPVCGLSTHTSGGRIIGGQPAKPG
                           RDS-
                                                                                                                                                                                          SM00032; CCP; 1.
m-binding; EGF-like domain; Glycoprotein;
                                                                                                   l Similarity
79; Conserv
                                                                                                                                                                                                                                                                                                                                                                    IPR000436; -.
IPR000561; -.
IPR000859; -.
                                                                                                                                                                623
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                                                                                                     Conservative
                                                                    ----QCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQH
                                                                                                                                                                ΑA;
                        GSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLV 165
                                                                                                                                                                    68568 MW;
                                                                                                                5.9%;
                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                     Score 123.5; DB 11,
Pred. No. 0.0082;
6; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                    233AF39E8906624F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 623
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                                                                                                                              DB 11;
      DFPWQVLLLGETTAAGALI
                                                                                                                                                                                              Repeat.
                                                                                                         Indels
                                                        -GKYVCEADGFWTSS
                                                                                                                                Length
                                                                                                          109;
                                                                                                                                 623;
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                                                                                                          Gaps
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Qy
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Q9QX84
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              δõ
                                                               Query Match
Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9QX84;
Q9QX84;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000152; ...
Interpro; IPR000436; ...
Interpro; IPR000561; ...
Interpro; IPR000739; ...
Interpro; IPR00059; ...
Interpro; IPR001254; ...
Interpro; IPR001314; ...
Interpro; IPR001314; ...
Interpro; IPR001381; ...
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                              PROSITE: PS00010; ASX_HYDROXYL; UPROSITE: PS01180; CUB: 2.
PROSITE: PS01186; EGF_2; 1.
PROSITE: PS01187; EGF_CA; 1.
PROSITE: PS01135; TRYPSIN_SER; 1.
SMART; SM00032; CCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y18572; CAB65389.1;
HSSP; P00736; 1APQ.
InterPro; IPR000152:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.;
"The Rat and mouse homologues of MASP-2 and MAp19, compo Mannan-Binding Lectin Activation Pathway of Complement." Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-FISHER 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: SECRETED (BY
-i- SIMILARITY: BELONGS TO THE INSULIN,
-i- SIMILARITY: TO CHYMOTRYPSIN SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316
                                                                                                                                                                              Calcium-binding;
NON_TER 1
SEQUENCE 643 A
                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00722; CHYMOTRYF PRINTS; PR00277; INSULINB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                   65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTHVPKGWIKGNANDIGMDYDYALLELKK--PHKRKEMKIGVSPPAKQLPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V--AGWGLTQKGFLARNLMFVDIPIVD-----HQKCATAYTKQPYPGAKVTVNMLCAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --FIHEGYTHG----AGFDNDIALIKLKNKVTINRNIMPICL--PRKEAASLMKTDFVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRGGKDSCRGDSGGALVFLDNETQRW--FVGGTVS---WGSINCGGSEQYGVYTKVT 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMN-GSPQDFNVAVRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IHFSGYDNDRPG----NLVYRFCDVKDETYDLLYQQC-----DAQPGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN (FRAGMENT).
                      CGP-
                                                                                        Similarity
                                                                                                                                                                                   643 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                    Conservative
-QCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAOH 115
                                                                                                                                                                                                                          EGF-like domain; Glycoprotein; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                     CHYMOTRYPSIN.
                                                                                                                                                                                     70976 MW;
                                                                                          5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECRETED (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                    ; Score 123.5;
; Pred. No. 0.0
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                        8164B9C0BF688CBB
                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   643
                                              0.0085;
3s 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  components nent.";
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (S1).
                                                                                   109;
                                                                                                                             643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus.
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RESULT
10 YX 61
10 YX
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO01254; -.
InterPro; IPRO01314; -.
Pfam; Pr00089; trypsin; 1.
PRINTS; PR00725; CHYMOTRYPSIN,
PROSITE; PS00134; TRYPSIN_HIS; U
PROSITE; PS00135; TRYPSIN_SER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
-i- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
EMBL; AF053919; AAD21839.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaines P.J., Sampson C.M., Rushlow K.E., "Cloning of a family of serine procease g Ctenocephalides felis.",
Insect Mol. Biol. 81:11-22(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ctenocephalides felis (Cat flea).
Eukaryota; Metazoa; Arthropoda; T
Pterygota; Neoptera; Endopterygot
Ctenocephalides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TIEMBLIFEL 12, C
01-NOV-1999 (TIEMBLIFEL 12, L
01-MAR-2001 (TIEMBLIFEL 16, L
TRYPSIN-LIKE SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9XY61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00020; Tryp_SPc;
Hydrolase; Protease; Seri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-99124360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9XY61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-7515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579
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  219
                                                                                                             159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431
                                                                                                                                                                                                                 101 VGIYILSS--SGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLST 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324
                                                      5<u>4</u>
                                                                                                                                                                11
                                                                                                                                                                VGLSAVSSYKIKDGLDGRIVGGQDADIAK---YGYQASLQVFNEHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRGGKDSCRGDSGGALVFLDNETQRW--FVGGIVS---WGSINCGGSEQYGVYTKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SGSGYYYRMWKRQQQKWERKIIGIFSGHQWVDMN-GSPQDFNVAVRIT
FQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V--AGWGLTQKGFLARNLMFVDIPIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IHFSGYDNDRPG----NLVYRFCDVKDETYDLLYQQC-----DAQPGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --FIHEGYTHG----AGFDNDIALIKLKNKVTINRNIMPICL--PRKEAASLMKTDFVGT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTHVPKGWIKGNANDIGMDYDYALLELKK--PHKRKFMKIGVSPPAKQLPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HDDWVLTAAHAVY-GKTEAMSSLDIRMGILK-----RLSLIYTQAWPEAV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVK 225
                                                                                                    GCTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGPPDDLPNGHVDYITGPEVTTYKAVIQYSCEETFYTMSSN-----GKYVCEADGFWTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGEKSLPVCKPVCGLSTHTSGGRIIGGQPAKPG------DFPWQVLLLGETTAAGALI 430
                                                -CGASILNNYWIVTAAHCIYDEFTY-----SVRVG---TSFQ-GRRGSVHPVAQIIKHPA 103
                                                                                                                                                                                                                                                                                                                                                                                                                    259
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed-9927170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLV 165
                                                                                                                                                                                                                                                                                                                                                                                                                 28299 MW;
                                                                                                                                                                                                                                                                                                       5.9%;
24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease
                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
E (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                       Score 122; DB 5;
Pred. No. 0.0034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              9B222E7EB430472A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNKNOWN_1
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracheata; Hexapoda; Insecta; 
ota; Siphonaptera; Pulicidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259
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                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                        Length 259
                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                          56;
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                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                             53
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RESULT
Q9VDU8
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                                                                                                                                                                                            RA Ballew R. M. Basu A., Aun. B. J., Audrews Fleminout C., Bearley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Dubbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyamm C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyamm C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Stypski M.P., Smith T.,
RA Soles B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stypski M.P., Smith T.,
RA Spier E., Johog F.N., Zhong W., Weinstock G.M., Weissenbach J.,
RA Yellon R., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Shou X., Smith H.O.,
RA Sible B.C., Siden Sequence of Drosophila melanogaster.";
RI Science 287:2186-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9VDU8;
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                    -i- SIMILARITY: TO SERINE PROTEASES,

-i- SIMILARITY: TO CHYMOTRYPSIN SERI

EMBL: AE003727; AAF55692.2; -

FlyBase; FBgn0038727; CG7432.
                                                                                                                                                                                      "The genome sequence of Dro
Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
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                       Pfam; PF00089; t
PRINTS; PR00722;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG7432 PROTEIN.
                                                            InterPro; IPR001254; -
InterPro; IPR001314; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 ELATVTGWGNLGEDEDDPEQLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
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  PS00134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY
                                          trypsin;
                     CHYMOTRYPSIN.
TRYPSIN_HIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10731132;
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16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
UNKNOWN_1.
                                                                                                                                               SERINE
                                                                                                                                                                  TRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449
                                                                                                                                               PROTEASE
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                                                                                                                                                                     FAMILY
                                                                                                                                                 FAMILY
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RESULT
ID 3207
AC Q6
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         Matches
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InterPro; IPRO00152; ...
InterPro; IPRO00294; ...
InterPro; IPRO00261; ...
InterPro; IPRO00742; ...
InterPro; IPRO00742; ...
InterPro; IPRO01254; ...
InterPro; IPRO01314; ...
InterPro; IPRO01381; ...
InterPro; IPRO01381; ...
InterPro; IPRO01881; ...
InterPro; IPRO01881; ...
InterPro; IPRO01881; ...
InterPro; IPRO0188; EGF; ...
Pfam; PF00008; EGF; ...
Pfam; PF000094; g1a; 1...
Pfam; PF000594; g1a; 1...
Pfam; PF000594; g1a; 1...
Pfam; PF000594; g1a; 1...
PRINTS; PR000722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
PRINTS; PR00001; GLABLOOD.
PROSITE; PS001186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q63207 PRELIMINARY; PKY;
Q63207;
Q153207;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last seq
Q1-MAR-2001 (TrEMBLrel. 16, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 CGGSLIGTKYILTAAHCTRDSRQKPFAARQFTVRLGDI------DLSTDAEPSDP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 CTGTLVAEKHVLTAAHCIHDG--KTYVKGTQKLRVGELKPKFKDGGRGANDSTSAMPEQM 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY:
MEDLINE-96093366; PubMed-8578539;
MEDLINE-96093366; PubMed-8578539;
Stanton C., Ross R.P., Hutson S., Wallin R.;
Stanton C., Ross R.P., Hutson S., Wallin R.;
Evidence for competition between vitamin K-dependent clotting factors
"Evidence for competition between vitamin K-dependent gamma-
for intracellular processing by the vitamin K-dependent gamma-
carboxylase.";
Thromb. Res. 80:63-73(1995).
Thromb. Res. 80:63-73(1995).
Thromb. Res. 80:63-73(1995).
SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
-1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 RLPGRRATVVGWGTTYYGGKESTSORQAELPIWR----NEDCDRSYFQPINENFICAGY 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 QLPG------GRIHFSGYD--NDRPGNL-VYRFCDVKDETYDLLYQQ------ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 VTFAVKEVRTH-----ERFSRIGFYNDIAILVLDKPVRKSKYVIPVCLPKGIRMPPKE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 KEQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGV-----SPPAK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 VAVRITPLKYAQICYWIKGNYLD
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les 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X79807; CAA56202.1;
HSSP; P00742; 1XKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDGGVDACQGDSGGPLMMR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYTRVT----EYLDWIRDHTRD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serine protease.
449 AA; 49331 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
            ; ASX_HYDROXYL; 1.; EGF_1; UNKNOWN_1.; EGF_2; 2.; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90DB193AA10D7331 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----YDSH-WVQLGVVSFGNKCGEPGYPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŗ
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DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00134; TRYPSIN_LIS; UNKNOWN_1.

DR PROSITE; PS00134; TRYPSIN_LIS; UNKNOWN_1.

EXAMPT; SMO020; TryP_SPC: 1.

EXAMPT SMO020; TryP_SPC: 1.

EXAMPT; SMO020; TryP_SPC: 1.

EXAMPT: 1.

EXA
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